

Please delete the paragraph on page 8, lines 5-7, and replace it with the following paragraph:

FIG. 1 is a schematic of various methods that may be employed to amplify VH genes without using primers specific for VH sequences. The T₁₅ oligonucleotide is shown in SEQ ID NO: 622.

Please delete the paragraph on page 8, lines 28-29, and replace it with the following paragraph:

FIG. 10 is a schematic of the design for CDR1 and CDR2 synthetic diversity. The YADSVKG peptide is shown in SEQ ID NO: 604.

Please delete the paragraph on page 9, lines 10-12, and replace it with the following paragraph:

FIG. 18 is a schematic of a process for incorporating fixed FR1 residues in an antibody lambda sequence. The PCRpr oligonucleotide is shown in SEQ ID NO: 605 while the Bridge oligonucleotide and encoded peptide are shown in SEQ ID NOS 606-607, respectively.

Please delete the paragraph on page 9, lines 13-15, and replace it with the following paragraph:

FIG. 19 is a schematic of a process for incorporating fixed FR1 residues in an antibody kappa sequence (see SEQ ID NOS 608-611, respectively, in order of appearance).

Please delete the paragraph on page 9, lines 16-18, and replace it with the following paragraph:

FIG. 20 is a schematic of a process for incorporating fixed FR1 residues in an antibody heavy chain sequence. The PCRpr oligonucleotide is shown in SEQ ID NO: 612. The Bridge

oligonucleotides are shown in SEQ ID NOS 613 & 615, respectively, in order of appearance, while the encoded peptides are shown in SEQ ID NOS 614 & 616, respectively, in order of appearance.

Please delete the paragraph on page 56, line 9, to page 57, line 3, and replace it with the following paragraph:

After bla, is the Fab cassette (illustrated in FIG. 17) comprising:

- a) PlacZ promoter,
- b) A first Ribosome Binding Site (RBS1),
- c) The signal sequence form M13 iii,
- d) An *ApaLI* RERS,
- e) A light chain (a kappa L20::JK1 shortened by one codon at the V-J boundary in this case),
- f) An *AscI* RERS,
- g) A second Ribosome Binding Site (RBS2),
- h) A signal sequence, preferably *PelB*, which contains,
- i) An *SfiI* RERS,
- j) A synthetic 3-23 V region with diversity in CDR1 and CDR2,
- k) A captured CDR3,
- l) A partially synthetic J region (FR4 after *BstEII*),
- m) CH1,
- n) A *NotI* RERS,
- o) A His6 tag (SEQ ID NO: 12),
- p) A cMyc tag,
- q) An amber codon,
- r) An anchor DNA that encodes the same amino-acid sequence as codons 273 to 424 of M13 iii (as shown in Table 37).
- s) Two stop codons,
- t) An *AvrII* RERS, and
- u) A trp terminator.

Please delete the paragraph on page 58, lines 6-16, and replace it with the following paragraph:

Table 38 shows a gene fragment comprising the *NotI* site, His6 tag (SEQ ID NO: 12), cMyc tag, an amber codon, a recombinant enterokinase cleavage site, and the whole of mature M13 III protein. The DNA used to encode this sequence is intentionally very different from the DNA of wild-type gene iii as shown by the lines denoted "W.T." containing the w.t. bases where these differ from this gene. III is divided into domains denoted "domain 1", "linker 1", "domain 2", "linker 2", "domain 3", "transmembrane segment", and "intracellular anchor".

Please delete the paragraph on page 59, lines 5-23, and replace it with the following paragraph:

The constructs would most readily be made by methods similar to those of Wang and Wilkinson (Biotechniques 2001: 31(4)722-724) in which PCR is used to copy the vector except the part to be deleted and matching restriction sites are introduced or retained at either end of the part to be kept. Table 39 shows the oligonucleotides to be used in deleting parts of the III anchor segment. The DNA shown in Table 38 has an *NheI* site before the DINDDRMA (residues 29-36 of SEQ ID NO: 594) recombinant enterokinase cleavage site (rEKCS). If *NheI* is used in the deletion process with this DNA, the rEKCS site would be lost. This site could be quite useful in cleaving Fabs from the phage and might facilitate capture of very high-affinity antibodies. One could mutagenize this sequence so that the *NheI* site would follow the rEKCS site, an Ala Ser amino-acid sequence is already present. Alternatively, one could use *SphI* for the deletions. This would involve a slight change in amino acid sequence but would be of no consequence.

Please delete Table 1 and replace it with the following table:

Table 1: Human GLG FR3 sequences
! VH1

! 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac atg
! 81 82 82a 82b 82c 83 84 85 86 87 88 89 90 91 92
gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt
! 93 94 95
gcg aga ga ! 1-02# 1 (SEQ ID NO: 34)
aga gtc acc att acc agg gac aca tcc gcg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat tac tgt
gcg aga ga ! 1-03# 2 (SEQ ID NO: 35)
aga gtc acc atg acc agg aac acc tcc ata agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga gg ! 1-08# 3 (SEQ ID NO: 36)
aga gtc acc atg acc aca gac aca tcc acg agc aca gcc tac atg
gag ctg agg agc ctg aga tct gac gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-18# 4 (SEQ ID NO: 37)
aga gtc acc atg acc gag gac aca tct aca gac aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gca aca ga ! 1-24# 5 (SEQ ID NO: 38)
aga gtc acc att acc agg gac agg tct atg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac aca gcc atg tat tac tgt
gca aga ta ! 1-45# 6 (SEQ ID NO: 39)
aga gtc acc atg acc agg gac acg tcc acg agc aca gtc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-46# 7 (SEQ ID NO: 40)
aga gtc acc att acc agg gac atg tcc aca agc aca gcc tac atg
gag ctg agc agc ctg aga tcc gag gac acg gcc gtg tat tac tgt
gcg gca ga ! 1-58# 8 (SEQ ID NO: 41)
aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-69# 9 (SEQ ID NO: 42)
aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 1-e# 10 (SEQ ID NO: 43)
aga gtc acc ata acc gcg gac acg tct aca gac aca gcc tac atg
gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt
gca aca ga ! 1-f# 11 (SEQ ID NO: 44)
! VH2
agg ctc acc atc acc aag gac acc tcc aaa aac cag gtg gtc ctt
aca atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt
gca cac aga c! 2-05# 12 (SEQ ID NO: 45)
agg ctc acc atc tcc aag gac acc tcc aaa agc cag gtg gtc ctt

acc atg acc aac atg gac cct gtg gac aca gcc aca tat tac tgt
gca cgg ata c! 2-26# 13 (SEQ ID NO: 46)

agg ctc acc atc tcc aag gac acc tcc aaa aac cag gtg gtc ctt
aca atg acc aac atg gac cct gtg gac aca gcc acg tat tac tgt
gca cgg ata c! 2-70# 14 (SEQ ID NO: 47)

! VH3

cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-07# 15 (SEQ ID NO: 48)

cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg
caa atg aac agt ctg aga gct gag gac acg gcc ttg tat tac tgt
gca aaa gat a! 3-09#16 (SEQ ID NO: 49)

cga ttc acc atc tcc agg gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 3-11# 17 (SEQ ID NO: 50)

cga ttc acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt
caa atg aac agc ctg aga gcc ggg gac acg gct gtg tat tac tgt
gca aga ga ! 3-13# 18 (SEQ ID NO: 51)

aga ttc acc atc tca aga gat gat tca aaa aac acg ctg tat ctg
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt
acc aca ga ! 3-15# 19 (SEQ ID NO: 52)

cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctg tat ctg
caa atg aac agt ctg aga gcc gag gac acg gcc ttg tat cac tgt
gcg aga ga ! 3-20# 20 (SEQ ID NO: 53)

cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-21# 21 (SEQ ID NO: 54)

cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt
gcg aaa ga ! 3-23# 22 (SEQ ID NO: 55)

cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aaa ga ! 3-30# 23 (SEQ ID NO: 56)

cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3303# 24 (SEQ ID NO: 57)

cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aaa ga ! 3305# 25 (SEQ ID NO: 58)

cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt

gcg aga ga ! 3-33# 26 (SEQ ID NO: 59)
cga ttc acc atc tcc aga gac aac agc aaa aac tcc ctg tat ctg
caa atg aac agt ctg aga act gag gac acc gcc ttg tat tac tgt
gca aaa gat a! 3-43#27 (SEQ ID NO: 60)
cga ttc acc atc tcc aga gac aat gcc aag aac tca ctg tat ctg
caa atg aac agc ctg aga gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-48# 28 (SEQ ID NO: 61)
aga ttc acc atc tca aga gat ggt tcc aaa agc atc gcc tat ctg
caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat tac tgt
act aga ga ! 3-49# 29 (SEQ ID NO: 62)
cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt
gcg aga ga ! 3-53# 30 (SEQ ID NO: 63)
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg ggc agc ctg aga gct gag gac atg gct gtg tat tac tgt
gcg aga ga ! 3-64# 31 (SEQ ID NO: 64)
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctt
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
gcg aga ga ! 3-66# 32 (SEQ ID NO: 65)
aga ttc acc atc tca aga gat gat tca aag aac tca ctg tat ctg
caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt
gct aga ga ! 3-72# 33 (SEQ ID NO: 66)
agg ttc acc atc tcc aga gat gat tca aag aac acg gcg tat ctg
caa atg aac agc ctg aaa acc gag gac acg gcc gtg tat tac tgt
act aga ca ! 3-73# 34 (SEQ ID NO: 67)
cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctg
caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt
gca aga ga ! 3-74# 35 (SEQ ID NO: 68)
aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg cat ctt
caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt
aag aaa ga ! 3-d# 36 (SEQ ID NO: 69)

! VH4

cga gtc acc ata tca gta gac aag tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt
gcg aga ga ! 4-04# 37 (SEQ ID NO: 70)
cga gtc acc atg tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gtg gac acg gcc gtg tat tac tgt
gcg aga aa ! 4-28# 38 (SEQ ID NO: 71)
cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg
aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt
gcg aga ga ! 4301# 39 (SEQ ID NO: 72)

cga gtc acc ata tca gta gac agg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gcg gac acg gcc gtg tat tac tgt
gcc aga ga ! 4302# 40 (SEQ ID NO: 73)

cga gtt acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg act gcc gca gac acg gcc gtg tat tac tgt
gcc aga ga ! 4304# 41 (SEQ ID NO: 74)

cga gtt acc ata tca gta gac acg tct aag aac cag ttc tcc ctg
aag ctg agc tct gtg act gcc gcg gac acg gcc gtg tat tac tgt
gca aga ga ! 4-31# 42 (SEQ ID NO: 75)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac tgt
gca aga ga ! 4-34# 43 (SEQ ID NO: 76)

cga gtc acc ata tcc gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac tgt
gca aga ca ! 4-39# 44 (SEQ ID NO: 77)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gct gca gac acg gct gtg tat tac tgt
gca aga ga ! 4-59# 45 (SEQ ID NO: 78)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gct gca gac acg gct gtg tat tac tgt
gca aga ga ! 4-61# 46 (SEQ ID NO: 79)

cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg
aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac tgt
gca aga ga ! 4-b# 47 (SEQ ID NO: 80)

! VH5

cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt
gca aga ca ! 5-51# 48 (SEQ ID NO: 81)

cac gtc acc atc tca gct gac aag tcc atc agc act gcc tac ctg
cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt
gca aga ga ! 5-a# 49 (SEQ ID NO: 82)

! VH6

cga ata acc atc aac cca gac aca tcc aag aac cag ttc tcc ctg
cag ctg aac tct gtg act ccc gag gac acg gct gtg tat tac tgt
gca aga ga ! 6-1# 50 (SEQ ID NO: 83)

! VH7

cggttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat ctg
cag atc tgc agc cta aag gct gag gac act gcc gtg tat tac tgt
gca aga ga ! 74.1# 51 (SEQ ID NO: 84)

Please delete Table 2 and replace it with the following table:

Table 2: Enzymes that either cut 15 or more human GLGs or have 5+-base recognition in FR3

Typical entry:

REname	Recognition	#sites				
GLGid#	:base#	GLGid#	:base#	GLGid#	:base#

BstEII Ggttnacc 2

1: 3 48: 3

There are 2 hits at base# 3

MaeIII gtnac 36

1: 4	2: 4	3: 4	4: 4	5: 4	6: 4
7: 4	8: 4	9: 4	10: 4	11: 4	37: 4
37: 58	38: 4	38: 58	39: 4	39: 58	40: 4
40: 58	41: 4	41: 58	42: 4	42: 58	43: 4
43: 58	44: 4	44: 58	45: 4	45: 58	46: 4
46: 58	47: 4	47: 58	48: 4	49: 4	50: 58

There are 24 hits at base# 4

Tsp45I gtsac 33

1: 4	2: 4	3: 4	4: 4	5: 4	6: 4
7: 4	8: 4	9: 4	10: 4	11: 4	37: 4
37: 58	38: 4	38: 58	39: 58	40: 4	40: 58
41: 58	42: 58	43: 4	43: 58	44: 4	44: 58
45: 4	45: 58	46: 4	46: 58	47: 4	47: 58
48: 4	49: 4	50: 58			

There are 21 hits at base# 4

HphI tcacc 45

1: 5	2: 5	3: 5	4: 5	5: 5	6: 5
7: 5	8: 5	11: 5	12: 5	12: 11	13: 5
14: 5	15: 5	16: 5	17: 5	18: 5	19: 5
20: 5	21: 5	22: 5	23: 5	24: 5	25: 5
26: 5	27: 5	28: 5	29: 5	30: 5	31: 5
32: 5	33: 5	34: 5	35: 5	36: 5	37: 5
38: 5	40: 5	43: 5	44: 5	45: 5	46: 5

47: 5 48: 5 49: 5

There are 44 hits at base# 5

NlaIII CATG		26					
1: 9	1: 42	2: 42	3: 9	3: 42	4: 9		
4: 42	5: 9	5: 42	6: 42	6: 78	7: 9		
7: 42	8: 21	8: 42	9: 42	10: 42	11: 42		
12: 57	13: 48	13: 57	14: 57	31: 72	38: 9		
48: 78	49: 78						

There are 11 hits at base# 42

There are 1 hits at base# 48 Could cause raggedness.

BsaJI Ccnnggg		37					
1: 14	2: 14	5: 14	6: 14	7: 14	8: 14		
8: 65	9: 14	10: 14	11: 14	12: 14	13: 14		
14: 14	15: 65	17: 14	17: 65	18: 65	19: 65		
20: 65	21: 65	22: 65	26: 65	29: 65	30: 65		
33: 65	34: 65	35: 65	37: 65	38: 65	39: 65		
40: 65	42: 65	43: 65	48: 65	49: 65	50: 65		
51: 14							

There are 23 hits at base# 65

There are 14 hits at base# 14

AluI AGct		42					
1: 47	2: 47	3: 47	4: 47	5: 47	6: 47		
7: 47	8: 47	9: 47	10: 47	11: 47	16: 63		
23: 63	24: 63	25: 63	31: 63	32: 63	36: 63		
<u>37: 47</u>	<u>37: 52</u>	<u>38: 47</u>	<u>38: 52</u>	<u>39: 47</u>	<u>39: 52</u>		
<u>40: 47</u>	<u>40: 52</u>	<u>41: 47</u>	<u>41: 52</u>	<u>42: 47</u>	<u>42: 52</u>		
<u>43: 47</u>	<u>43: 52</u>	<u>44: 47</u>	<u>44: 52</u>	<u>45: 47</u>	<u>45: 52</u>		
<u>46: 47</u>	<u>46: 52</u>	<u>47: 47</u>	<u>47: 52</u>	<u>49: 15</u>	<u>50: 47</u>		

There are 23 hits at base# 47

There are 11 hits at base# 52 Only 5 bases from 47

BspI GCtnagc		21					
1: 48	2: 48	3: 48	5: 48	6: 48	7: 48		
8: 48	9: 48	10: 48	11: 48	37: 48	38: 48		
39: 48	40: 48	41: 48	42: 48	43: 48	44: 48		
45: 48	46: 48	47: 48					

There are 21 hits at base# 48

MwoI GCNNNNnngc (SEQ ID NO: 85) 19

1: 48	2: 28	19: 36	22: 36	23: 36	24: 36
25: 36	26: 36	35: 36	37: 67	39: 67	40: 67
41: 67	42: 67	43: 67	44: 67	45: 67	46: 67
47: 67					

There are 10 hits at base# 67

There are 7 hits at base# 36

DdeI Ctnag

71

1: 49	1: 58	2: 49	2: 58	3: 49	3: 58
3: 65	4: 49	4: 58	5: 49	5: 58	5: 65
6: 49	<u>6: 58</u>	<u>6: 65</u>	7: 49	<u>7: 58</u>	7: 65
8: 49	8: 58	9: 49	<u>9: 58</u>	<u>9: 65</u>	10: 49
<u>10: 58</u>	<u>10: 65</u>	11: 49	<u>11: 58</u>	<u>11: 65</u>	15: 58
<u>16: 58</u>	<u>16: 65</u>	17: 58	18: 58	20: 58	21: 58
22: 58	<u>23: 58</u>	<u>23: 65</u>	<u>24: 58</u>	24: 65	<u>25: 58</u>
<u>25: 65</u>	26: 58	<u>27: 58</u>	<u>27: 65</u>	28: 58	30: 58
<u>31: 58</u>	<u>31: 65</u>	<u>32: 58</u>	<u>32: 65</u>	35: 58	<u>36: 58</u>
<u>36: 65</u>	37: 49	38: 49	39: 26	39: 49	40: 49
41: 49	42: 26	42: 49	43: 49	44: 49	45: 49
46: 49	47: 49	48: 12	49: 12	51: 65	

There are 29 hits at base# 58

There are 22 hits at base# 49 Only nine base from 58

There are 16 hits at base# 65 Only seven bases from 58

BglII Agatct

11

1: 61	2: 61	3: 61	4: 61	5: 61	6: 61
7: 61	9: 61	10: 61	11: 61	51: 47	

There are 10 hits at base# 61

BstYI Rgatcy

12

1: 61	2: 61	3: 61	4: 61	5: 61	6: 61
7: 61	8: 61	9: 61	10: 61	11: 61	51: 47

There are 11 hits at base# 61

Hpy188I TCNGa

17

1: 64	2: 64	3: 64	4: 64	5: 64	6: 64
7: 64	8: 64	9: 64	10: 64	11: 64	16: 57
20: 57	27: 57	35: 57	48: 67	49: 67	

There are 11 hits at base# 64

There are 4 hits at base# 57

There are 2 hits at base# 67 Could be ragged.

MsII CAYNNnnRTG (SEQ_ID NO:86) 44

1: 72	2: 72	3: 72	4: 72	5: 72	6: 72
7: 72	8: 72	9: 72	10: 72	11: 72	15: 72
17: 72	18: 72	19: 72	21: 72	23: 72	24: 72
25: 72	26: 72	28: 72	29: 72	30: 72	31: 72
32: 72	33: 72	34: 72	35: 72	36: 72	37: 72
38: 72	39: 72	40: 72	41: 72	42: 72	43: 72
44: 72	45: 72	46: 72	47: 72	48: 72	49: 72
50: 72	51: 72				

There are 44 hits at base# 72

BsiEI CGRYcg

23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

EaeI Yggccr

23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

EagI Cggccg

23

1: 74	3: 74	4: 74	5: 74	7: 74	8: 74
9: 74	10: 74	11: 74	17: 74	22: 74	30: 74
33: 74	34: 74	37: 74	38: 74	39: 74	40: 74
41: 74	42: 74	45: 74	46: 74	47: 74	

There are 23 hits at base# 74

HaeIII GGcc 27

1: 75	3: 75	4: 75	5: 75	7: 75	8: 75
9: 75	10: 75	11: 75	16: 75	17: 75	20: 75
22: 75	30: 75	33: 75	34: 75	37: 75	38: 75
39: 75	40: 75	41: 75	42: 75	45: 75	46: 75
47: 75	48: 63	49: 63			

There are 25 hits at base# 75

Bst4CI ACNgt 65°C 63 Sites There is a third isoschism

1: 86	2: 86	3: 86	4: 86	5: 86	6: 86
7: 34	7: 86	8: 86	9: 86	10: 86	11: 86
12: 86	13: 86	14: 86	15: 36	15: 86	16: 53
16: 86	17: 36	17: 86	18: 86	19: 86	20: 53
20: 86	21: 36	21: 86	22: 0	22: 86	23: 86
24: 86	25: 86	26: 86	27: 53	27: 86	28: 36
28: 86	29: 86	30: 86	31: 86	32: 86	33: 36
33: 86	34: 86	35: 53	35: 86	36: 86	37: 86
38: 86	39: 86	40: 86	41: 86	42: 86	43: 86
44: 86	45: 86	46: 86	47: 86	48: 86	49: 86
50: 86	51: 0	51: 86			

There are 51 hits at base# 86 All the other sites are well away

HpyCH4III ACNgt 63

1: 86	2: 86	3: 86	4: 86	5: 86	6: 86
7: 34	7: 86	8: 86	9: 86	10: 86	11: 86
12: 86	13: 86	14: 86	15: 36	15: 86	16: 53
16: 86	17: 36	17: 86	18: 86	19: 86	20: 53
20: 86	21: 36	21: 86	22: 0	22: 86	23: 86
24: 86	25: 86	26: 86	27: 53	27: 86	28: 36
28: 86	29: 86	30: 86	31: 86	32: 86	33: 36
33: 86	34: 86	35: 53	35: 86	36: 86	37: 86
38: 86	39: 86	40: 86	41: 86	42: 86	43: 86
44: 86	45: 86	46: 86	47: 86	48: 86	49: 86
50: 86	51: 0	51: 86			

There are 51 hits at base# 86

HinfI Gantc 43

2:	2	3:	2	4:	2	5:	2	6:	2	7:	2
8:	2	9:	2	9:	22	10:	2	11:	2	15:	2
16:	2	17:	2	18:	2	19:	2	19:	22	20:	2
21:	2	23:	2	24:	2	25:	2	26:	2	27:	2
28:	2	29:	2	30:	2	31:	2	32:	2	33:	2
33:	22	34:	22	35:	2	36:	2	37:	2	38:	2
40:	2	43:	2	44:	2	45:	2	46:	2	47:	2
50:	60										

There are 38 hits at base# 2

MlyI GAGTCNNNNNN (SEQ ID NO:87) 18

2:	2	3:	2	4:	2	5:	2	6:	2	7:	2
8:	2	9:	2	10:	2	11:	2	37:	2	38:	2
40:	2	43:	2	44:	2	45:	2	46:	2	47:	2

There are 18 hits at base# 2

PleI gagtc 18

2:	2	3:	2	4:	2	5:	2	6:	2	7:	2
8:	2	9:	2	10:	2	11:	2	37:	2	38:	2
40:	2	43:	2	44:	2	45:	2	46:	2	47:	2

There are 18 hits at base# 2

AciI Ccgc 24

2:	26	9:	14	10:	14	11:	14	27:	74	<u>37:</u>	<u>62</u>
<u>37:</u>	<u>65</u>	38:	62	39:	65	<u>40:</u>	<u>62</u>	40:	65	41:	65
42:	65	<u>43:</u>	<u>62</u>	<u>43:</u>	<u>65</u>	<u>44:</u>	<u>62</u>	<u>44:</u>	<u>65</u>	45:	62
46:	62	<u>47:</u>	<u>62</u>	<u>47:</u>	<u>65</u>	48:	35	48:	74	49:	74

There are 8 hits at base# 62

There are 8 hits at base# 65

There are 3 hits at base# 14

There are 3 hits at base# 74

There are 1 hits at base# 26

There are 1 hits at base# 35

-" - Gcgg 11

8:	91	9:	16	10:	16	11:	16	37:	67	39:	67
40:	67	42:	67	43:	67	45:	67	46:	67		

There are 7 hits at base# 67

There are 3 hits at base# 16

There are 1 hits at base# 91

BsiHKAI GWGCWc 20
2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
46: 51 47: 51

There are 11 hits at base# 51

Bsp1286I GDGCHC 20
2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
46: 51 47: 51

There are 11 hits at base# 51

HgiAI GWGCWc 20
2: 30 4: 30 6: 30 7: 30 9: 30 10: 30
12: 89 13: 89 14: 89 37: 51 38: 51 39: 51
40: 51 41: 51 42: 51 43: 51 44: 51 45: 51
46: 51 47: 51

There are 11 hits at base# 51

BsoFI GCngc 26
2: 53 3: 53 5: 53 6: 53 7: 53 8: 53
8: 91 9: 53 10: 53 11: 53 31: 53 36: 36
37: 64 39: 64 40: 64 41: 64 42: 64 43: 64
44: 64 45: 64 46: 64 47: 64 48: 53 49: 53
50: 45 51: 53

There are 13 hits at base# 53

There are 10 hits at base# 64

TseI Gcwgc 17
2: 53 3: 53 5: 53 6: 53 7: 53 8: 53
9: 53 10: 53 11: 53 31: 53 36: 36 45: 64
46: 64 48: 53 49: 53 50: 45 51: 53
There are 13 hits at base# 53

MnII gagg 34

3: 67	3: 95	4: 51	5: 16	5: 67	6: 67
7: 67	8: 67	9: 67	10: 67	11: 67	15: 67
16: 67	17: 67	19: 67	20: 67	21: 67	22: 67
23: 67	24: 67	25: 67	26: 67	27: 67	28: 67
29: 67	30: 67	31: 67	32: 67	33: 67	34: 67
35: 67	36: 67	50: 67	51: 67		

There are 31 hits at base# 67

HpyCH4V TGca 34

5: 90	6: 90	11: 90	12: 90	13: 90	14: 90
15: 44	16: 44	16: 90	17: 44	18: 90	19: 44
20: 44	21: 44	22: 44	23: 44	24: 44	25: 44
26: 44	27: 44	27: 90	28: 44	29: 44	33: 44
34: 44	35: 44	35: 90	36: 38	48: 44	49: 44
50: 44	50: 90	51: 44	51: 52		

There are 21 hits at base# 44

There are 1 hits at base# 52

AccI GTmkac 13 5-base recognition

7: 37	11: 24	37: 16	38: 16	39: 16	40: 16
41: 16	42: 16	43: 16	44: 16	45: 16	46: 16
47: 16					

There are 11 hits at base# 16

SacII CCGCgg 8 6-base recognition

9: 14	10: 14	11: 14	37: 65	39: 65	40: 65
42: 65	43: 65				

There are 5 hits at base# 65

There are 3 hits at base# 14

TfiI Gawtc 24

9: 22	15: 2	16: 2	17: 2	18: 2	19: 2
19: 22	20: 2	21: 2	23: 2	24: 2	25: 2
26: 2	27: 2	28: 2	29: 2	30: 2	31: 2
32: 2	33: 2	33: 22	34: 22	35: 2	36: 2

There are 20 hits at base# 2

BsmAI Nnnnnnngagac (SEQ ID NO:88) 19

15: 11 16: 11 20: 11 21: 11 22: 11 23: 11
24: 11 25: 11 26: 11 27: 11 28: 11 28: 56
30: 11 31: 11 32: 11 35: 11 36: 11 44: 87
48: 87

There are 16 hits at base# 11

BpmI ctccag 19

15: 12 16: 12 17: 12 18: 12 20: 12 21: 12
22: 12 23: 12 24: 12 25: 12 26: 12 27: 12
28: 12 30: 12 31: 12 32: 12 34: 12 35: 12
36: 12

There are 19 hits at base# 12

XmnI GAANNnnttc (SEQ ID NO:89) 12

37: 30 38: 30 39: 30 40: 30 41: 30 42: 30
43: 30 44: 30 45: 30 46: 30 47: 30 50: 30

There are 12 hits at base# 30

BsrI NCcagt 12

37: 32 38: 32 39: 32 40: 32 41: 32 42: 32
43: 32 44: 32 45: 32 46: 32 47: 32 50: 32

There are 12 hits at base# 32

BanII GRGCYc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

Ecl136I GAGctc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

SacI GAGCTc 11

37: 51 38: 51 39: 51 40: 51 41: 51 42: 51
43: 51 44: 51 45: 51 46: 51 47: 51

There are 11 hits at base# 51

Please delete Table 3 and replace it with the following table:

Table 3: Synthetic 3-23 FR3 of human heavy chains showing positions of possible cleavage sites

! Sites engineered into the synthetic gene are shown in upper case DNA
! with the RE name between vertical bars (as in | XbaI |).
! RERSSs frequently found in GLGs are shown below the synthetic sequence
! with the name to the right (as in gtn ac=MaeIII(24), indicating that
! 24 of the 51 GLGs contain the site).
!
!
! |---FR3---
! 89 90 (codon # in
! R F synthetic 3-23)
|cgc|ttc| 6
|cgn|tty|
|agr|
ga ntc = HinfI(38)
ga gtc = PleI(18)
ga wtc = TfiI(20)
gtn ac = MaeIII(24)
gts ac = Tsp45I(21)
tc acc = HphI(44)
!
! -----FR3-----
! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! T I S R D N S K N T L Y L Q M
(SEQ ID NO: 91)
|act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg| 51
!allowed|acn|ath|tcn|cgn|gay|aay|tcn|aar|aay|acn|ttr|tay|ttr|car|atg|

(SEQ ID NO: 90)
! |agy|agr| |agy| |ctn| |ctn|
! | ga|gac = BsmAI(16) | ag ct = AluI(23)
! c|tcc ag = BpmI(19) | g ctn agc = BlpI(21)
! | | g aan nnn ttc = XmnI(12)
! | XbaI | tg ca = HpyCH4V(21)
!
! -----FR3----->|
! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! N S L R A E D T A V Y Y C A K
|aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa| 96
!allowed|aay|tcn|ttr|cgn|gcn|gar|gay|acn|gcn|gtn|tay|tay|tgy|gcn|aar|
! |agy|ctn|agr| | | |

```

!           |   cc nng g = BsaJI(23)      ac ngt = Bst4CI(51)
!           |   aga tct = BglII(10)      ac ngt = HpyCH4III(51)
!           |   Rga tcY = BstYI(11)      ac ngt = TaaI(51)
!           |           c ayn nnn rtc = MsI(44)
!           |           cg ryc g = BsiEI(23)
!           |           yg gcc r = EaeI(23)
!           |           cg gcc g = EagI(23)
!           |           |g gcc = HaeIII(25)
!           |           gag g = MnI(31) |
!           |AflII |           | PstI |

```

Please delete Table 4 and replace it with the following table:

Table 4: REadaptors, Extenders, and Bridges used for Cleavage and Capture of Human Heavy Chains in FR3.

A: HpyCH4V Probes of actual human HC genes (SEQ ID NOS 92-100, respectively, in order of appearance)

HpyCH4V in FR3 of human HC, bases 35-56; only those with TGca site
TGca;10,
RE recognition:tgca of length 4 is expected at 10
 1 6-1 **agttctccctgcagctgaactc**
 2 3-11,3-07,3-21,3-72,3-48 **cactgtatctgcaaatgaacag**
 3 3-09,3-43,3-20 **ccctgtatctgcaaatgaacag**
 4 5-51 **ccgcctacctgcagtggagcag**
 5 3-15,3-30,3-30.5,3-30.3,3-74,3-23,3-33 **cgtgtatctgcaaatgaacag**
 6 7-4.1 **cggcatatctgcagatctgcag**
 7 3-73 **cggcgtatctgcaaatgaacag**
 8 5-a **ctgcctacctgcagtggagcag**
 9 3-49 **tcgcctatctgcaaatgaacag**

B: HpyCH4V REadaptors, Extenders, and Bridges

B.1 REadaptors

Cutting HC lower strand:

TmKeller for 100 mM NaCl, zero formamide

SEQ

Edapters for cleavage

T_m^W

T_m^K

ID NO:

(ON_HCFR36-1)

5'-agttctccctGCAGctgaactc-3'

68.0 64.5

92

(ON_HCFR36-1A)

5'-ttctcccTGCAGctgaactc-3'

62.0 62.5

residues

3-22 of 92

(ON_HCFR36-1B) 5'-ttctcccTGCAgctgaac-3' 56.0 59.9 residues
3-20 of 92

(ON_HCFR33-15) 5'-cgctgtatcTGCAaatgaacag-3' 64.0 60.8 96

(ON_HCFR33-15A) 5'-ctgtatcTGCAaatgaacag-3' 56.0 56.3 residues
3-22 of 96

(ON_HCFR33-15B) 5'-ctgtatcTGCAaatgaac-3' 50.0 53.1 residues
3-20 of 96

(ON_HCFR33-11) 5'-cactgtatcTGCAaatgaacag-3' 62.0 58.9 93

(ON_HCFR35-51) 5'-ccgcctaccTGCAgtggagcag-3' 74.0 70.1 95

!

B.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned

! XbaI... (SEQ ID NO: 101)

! D323* cgCttcacTaag tcT aga gac aaC tcT aag aaT acT ctC taC
! scab..... designed gene 3-23 gene.....

!

! HpyCH4V

! ... AflIII...

! Ttg caG atg aac agc TtA agG . . .

!

!

B.3 Extender and Bridges

! Extender (bottom strand):

! (SEQ ID NO: 102)

(ON_HCHpyEx01) 5'-cAAgTAgAgAgTATTcTTAgAgTTgTcTcTAgAcTTAgTgAAgcg-3'

! ON_HCHpyEx01 is the reverse complement of

! 5'-cgCttcacTaag tcT aga gac aaC tcT aag aaT acT ctC taC Ttg -3'

!

! Bridges (top strand, 9-base overlap):

! (SEQ ID NO: 103)

(ON_HCHpyBr016-1) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-
aaT acT ctC taC Ttg CAgctgaac-3' {3'-term C is blocked}

!

! 3-15 et al. + 3-11 (SEQ ID NO: 104)

(ON_HCHpyBr023-15) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-

aaT acT ctC taC Ttg CAaatgaac-3' {3'-term C is blocked}

!

! 5-51

(SEQ ID NO: 105)

(ON_HCHpyBr045-51) 5'-cgCttcacTaag tcT aga gac aaC tcT aag-
aaT acT ctC taC Ttg CAgtggagc-3' {3'-term C is blocked}

!

! PCR primer (top strand)

!

(ON_HCHpyPCR) 5'-cgCttcacTaag tcT aga gac-3' (SEQ ID NO: 106)

!

C: *B*lpI Probes from human HC GLGs

1	1-58,1-03,1-08,1-69,1-24,1-45,1-46,1-f,1-e	acatggaGCTGAGCaggcctgag
<u>(SEQ ID NO: 107)</u>		
2		1-02 acatggaGCTGAGCaggcctgag
<u>(SEQ ID NO: 108)</u>		
3		1-18 acatggagctgaggagcctgag
<u>(SEQ ID NO: 109)</u>		
4		5-51,5-a acctgcagtggagcaggcctgaa
<u>(SEQ ID NO: 110)</u>		
5	3-15,3-73,3-49,3-72	atctgcaaataaacagcctgaa
<u>(SEQ ID NO: 111)</u>		
6	3303,3-33,3-07,3-11,3-30,3-21,3-23,3305,3-48	atctgcaaataaacagcctgag
<u>(SEQ ID NO: 112)</u>		
7	3-20,3-74,3-09,3-43	atctgcaaataaacagtctgag
<u>(SEQ ID NO: 113)</u>		
8		74.1 atctgcagatctgcaggcctaaa
<u>(SEQ ID NO: 114)</u>		
9	3-66,3-13,3-53,3-d	atcttcaaataaacagcctgag
<u>(SEQ ID NO: 115)</u>		
10		3-64 atcttcaaataggcaggcctgag
<u>(SEQ ID NO: 116)</u>		
11	4301,4-28,4302,4-04,4304,4-31,4-34,4-39,4-59,4-61,4-b	ccctgaaGCTGAGCtctgtgac
<u>(SEQ ID NO: 117)</u>		
12		6-1 ccctgcagctgaactctgtgac
<u>(SEQ ID NO: 118)</u>		
13		2-70,2-05 tccttacaataccaaatgga
<u>(SEQ ID NO: 119)</u>		
14		2-26 tccttaccatgaccaacatgga
<u>(SEQ ID NO: 120)</u>		

D: BlpI REdapters, Extenders, and Bridges

D.1 REdapters

		T_m^W	T_mK
<u>(SEQ ID NO: 121)</u>			
(BlpF3HC1-58)	5'-ac atg gaG CTG AGC agc ctg ag-3'	70	66.4
<u>(SEQ ID NO: 122)</u>			
(BlpF3HC6-1)	5'-cc ctg aag ctg agc tct gtg ac-3'	70	66.4
! BlpF3HC6-1 matches 4-30.1, not 6-1.			

D.2 Segment of synthetic 3-23 gene into which captured CDR3 is to be cloned

!
BlpI
!
 XbaI...
...
!D323* cgCttcacTaag TCT AGA gac aaC tcT aag aaT acT ctC taC Ttg caG atg
aac
(SEQ ID NO: 123)!
!
 AflII...
!
 agC TTA AGG

D.3 Extender and Bridges

! Bridges
(BlpF3Br1) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-
 taC Ttg caG Ctg a|GC agc ctg-3' (SEQ ID NO: 124)
(BlpF3Br2) 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG-
 taC Ttg caG Ctg a|gc tct gtg-3' (SEQ ID NO: 125)
!
 | lower strand is cut here
! Extender
(BlpF3Ext) 5'-TcAgcTgcAAGTAcAAAAGTATTTTAcTgTTATcTcTAgAcTgAgTgAAgcg-3' (SEQ ID NO: 126)
! BlpF3Ext is the reverse complement of:
! 5'-cgCttcacTcag tcT aga gaT aaC AGT aaA aaT acT TtG taC Ttg caG Ctg a-3'
!
(BlpF3PCR) 5'-cgCttcacTcag tcT aga gaT aaC-3' (SEQ ID NO: 127)

E: HpyCH4III Distinct GLG sequences surrounding site, bases 77-98

1	102#1, 118#4, 146#7, 169#9, 1e#10, 311#17, 353#30, 404#37, 4301	ccgtgtattactgtgcgagaga
<u>(SEQ ID NO: 128)</u>		
2	103#2, 307#15, 321#21, 3303#24, 333#26, 348#28, 364#31, 366#32	ctgtgtattactgtgcgagaga
<u>(SEQ ID NO: 129)</u>		
3		108#3 ccgtgtattactgtgcgagagg
<u>(SEQ ID NO: 130)</u>		
4		124#5, 1f#11 ccgtgtattactgtgcaacaga
<u>(SEQ ID NO: 131)</u>		
5		145#6 ccatgtattactgtgcaagata
<u>(SEQ ID NO: 132)</u>		
6		158#8 ccgtgtattactgtgcggcaga
<u>(SEQ ID NO: 133)</u>		
7		205#12 ccacatattactgtgcacacag
<u>(SEQ ID NO: 134)</u>		
8		226#13 ccacatattactgtgcacggat
<u>(SEQ ID NO: 135)</u>		
9		270#14 ccacgtattactgtgcacggat
<u>(SEQ ID NO: 136)</u>		
10		309#16, 343#27 ctttgtattactgtgcaaaaga
<u>(SEQ ID NO: 137)</u>		
11		313#18, 374#35, 61#50 ctgtgtattactgtgcaagaga
<u>(SEQ ID NO: 138)</u>		
12		315#19 ccgtgtattactgttaccacaga
<u>(SEQ ID NO: 139)</u>		
13		320#20 ctttgtatcactgtgcgagaga
<u>(SEQ ID NO: 140)</u>		
14		323#22 ccgtatattactgtgcgaaaga
<u>(SEQ ID NO: 141)</u>		
15		330#23, 3305#25 ctgtgtattactgtgcgaaaga
<u>(SEQ ID NO: 142)</u>		
16		349#29 ccgtgtattactgtactagaga
<u>(SEQ ID NO: 143)</u>		
17		372#33 ccgtgtattactgtgctagaga
<u>(SEQ ID NO: 144)</u>		
18		373#34 ccgtgtattactgtactagaca
<u>(SEQ ID NO: 145)</u>		
19		3d#36 ctgtgtattactgtaaagaaaga
<u>(SEQ ID NO: 146)</u>		
20		428#38 ccgtgtattactgtgcgagaaa
<u>(SEQ ID NO: 147)</u>		
21		4302#40, 4304#41 ccgtgtattactgtgccagaga
<u>(SEQ ID NO: 148)</u>		
22		439#44 ctgtgtattactgtgcgagaca
<u>(SEQ ID NO: 149)</u>		
23		551#48 ccatgtattactgtgcgagaca
<u>(SEQ ID NO: 150)</u>		
24		5a#49 ccatgtattactgtgcgaga
<u>(SEQ ID NO: 151)</u>		

F: HpyCH4III REDaptors, Extenders, and Bridges

F.1 REDaptors

(SEQ ID NOS 152-159, respectively, in order of appearance)

! ONs for cleavage of HC(lower) in FR3 (bases 77-97)

! For cleavage with HpyCH4III, Bst4CI, or XbaI

! cleavage is in lower chain before base 88.

!
77 788 888 888 889 999 999 9

!
78 901 234 567 890 123 456 7 T_m^W

T_m^K

(H43.77.97.1-02#1)	5'-cc gtg tat tAC TGT gcg aga g-3'	6462.6
(H43.77.97.1-03#2)	5'-ct gtg tat tAC TGT gcg aga g-3'	6260.6
(H43.77.97.108#3)	5'-cc gtg tat tAC TGT gcg aga g-3'	6462.6
(H43.77.97.323#22)	5'-cc gta tat tac tgt gcg aaa g-3'	6058.7
(H43.77.97.330#23)	5'-ct gtg tat tac tgt gcg aaa g-3'	6058.7
(H43.77.97.439#44)	5'-ct gtg tat tac tgt gcg aga c-3'	6260.6
(H43.77.97.551#48)	5'-cc atg tat tac tgt gcg aga c-3'	6260.6
(H43.77.97.5a#49)	5'-cc atg tat tAC TGT gcg aga -3'	5858.3

F.2 Extender and Bridges

! XbaI and AflII sites in bridges are bunged

(H43.XABr1) 5'-ggtgttagtga-

| TCT|AGt|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
| aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aga-3'

(SEQ ID NO: 160)

(H43.XABr2) 5'-ggtgttagtga-

| TCT|AGt|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
| aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgt|gcg|aaa-3'

(SEQ ID NO: 161)

(H43.XAEext) 5'-ATAgTAgAcT gcAgTgTccT cAgcccTTAA gcTgTTcATc TgcAAgTAgA-
gAgTATTcTT AgAgTTgTcT cTAgATcAcT AcAcc-3' **(SEQ ID NO: 162)**

! H43.XAEext is the reverse complement of

! 5'-ggtgttagtga-

! | TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
! | aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat| -3'

(H43.XAPCR) 5'-ggtgttagtga |TCT|AGA|gac|aac-3' **(SEQ ID NO: 163)**

! XbaI and AflII sites in bridges are bunged

(H43.ABr1) 5'-ggtgttagtga-

| aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat tgt gcg aga-3'
(SEQ ID NO: 164)

(H43.ABr2) 5'-ggtgttagtga-
| aac|agC|TTt|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat tgt gcg aaa-3'
(SEQ ID NO: 165)

(H43.AExt) 5'-ATAgTAgActTgcAgTgTccTcAgcccTTAAgcTgTTTcAcTAcAcc-3'
(SEQ ID NO: 166)

! (H43.AExt) is the reverse complement of 5'-ggtgttagtga-
! | aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat -3' (SEQ ID NO: 167)
(H43.APCR) 5'-ggtgttagtga | aac|agC|TTA|AGg|gct|g-3' (SEQ ID NO: 168)

Please delete Table 5 and replace it with the following table:

Table 5: Analysis of frequency of matching REdantors in actual V genes

A: HnvsCH4V in HC at basses 35-56

Number of mismatches.....											Number				
Id	Ntot	0	1	2	3	4	5	6	7	8	9	10	Cut	Id	Probe
1	510	5	11	274	92	61	25	22	11	1	3	5	443	6-1	aggttctccctGGCAGctgaaactc
2	192	54	42	32	24	15	2	3	10	3	1	6	167	3-11	cactgttatctTGCAaatgaaacag
3	58	19	7	17	6	5	1	0	1	0	2	0	54	3-09	ccctgttatctTGCAaatgaaacag
4	267	42	33	9	8	8	82	43	22	8	11	1	100	5-51	cggcctacatcTGCAAGtgtggagg
5	250	111	59	41	24	7	5	1	0	0	2	0	242	3-15	cgtctgttatctTGCAaatgaaacag
6	7	0	2	0	1	0	0	0	0	0	4	0	3	7-4-1	cggcatatcTGCAAGatctgca
7	7	0	2	2	0	0	2	1	0	0	0	0	4	3-73	cggcgttatctTGCAaatgaaacag
8	26	10	4	1	3	1	2	1	3	1	0	0	19	5-a	ctgcctacatcTGCAAGtgtggagg
9	21	8	2	3	1	6	1	0	0	0	0	0	20	3-49	tgcctatctTGCAaatgaaacag
1338	249	162	379	149	103	120	71	47	13	23	12	1052	.	<u>(SEQ ID NOS 169-177,</u>	
	249	411	790	939	1162	1280	1316							<u>respectively in order</u>	
		1042		1233										<u>of appearance)</u>	

of appearance)

Id	Probe	dotted probe
6-1	agttctccCTGCAGctgaactc	aggttctccCTGCAGctgaactc
3-11	cactgtatcTGCAaatgaacag	cac.g.at.....aa.....ag
3-09	ccctgtatcTGCAaatgaacag	ccc.g.at.....aa.....ag
5-51	ccgcctacacTGCAgtggaggcag	ccgc..a.....tq..g.ag

3-15	cgctgtatctGCAaatgaacag	c.c.g.at.....aa.....ag
7-4..1	cgccatatctGCAGatctgcag	c.gca.at.....a.ctg.ag
3-73	cggcgtatctGCAaatgaacag	c.gcg.at.....aa.....ag
5-a	ctgcctacctGCAGtgaggcag	ctgc..a.....tg..g.ag
3-49	tgcgcatatctGCAaatgaacag	tcgc..at.....aa.....ag

(SEQ ID NOS 169-177, respectively in order of appearance)

Seqs with the expected RE site only.....1004

(Counts only cases with 4 or fewer mismatches)

Seqs with only an unexpected site.....0

Seqs with both expected and unexpected.... 48

(Counts only cases with 4 or fewer mismatches)

Seqs with no sites.....0

B: BpI in HC

Id	Ntot	0	1	2	3	4	5	6	7	8	Ncut	Name
1	133	73	16	11	13	6	9	1	4	0	119	1-58
2	14	11	1	0	0	0	1	0	1	12	1-02	acatggAGCTGAGCAGCCTGAG
3	34	17	8	2	6	1	0	0	0	0	1-18	acatggAGCTGAGCAGCCTGAG
4	120	50	32	16	10	9	1	1	1	0	2	5-51
5	55	13	11	10	17	3	1	0	0	0	0	3-15
6	340	186	88	41	15	6	3	0	1	0	0	3303
7	82	25	16	25	12	1	3	0	0	0	0	3-20
8	3	0	2	0	1	0	0	0	0	0	0	74..1
9	23	18	2	2	1	0	0	0	0	0	0	3-66
10	2	1	0	1	0	0	0	0	0	0	0	3-64

<u>(SEQ ID NOS 178-191), respectively in order of appearance)</u>										
Name	Full sequence					Dot mode				
1-58	a	c	t	g	a	g	c	t	G	AGG
1-02	a	c	t	g	g	a	g	c	t	g
1-18	a	c	t	g	g	a	g	c	t	g
5-51	a	c	t	g	g	a	g	c	t	g
3-15	a	t	c	g	a	a	c	a	a	a
3-30.3	a	t	c	t	g	a	a	c	a	a
3-20	a	t	c	t	g	a	a	c	a	t
7-4.1	a	t	c	g	a	g	c	a	c	a
3-66	a	t	c	a	a	c	t	t	c	a
3-64	a	t	c	t	a	g	c	t	t	g
4-30.1	c	c	t	g	a	g	c	t	c	t
6-1	c	c	t	g	a	g	c	c	a	t
2-70	t	c	t	c	a	a	c	t	a	c
2-26	t	c	t	c	c	a	c	a	a	g

Seqs with the expected RE site only..... 597 (counting sequences with 4 or fewer mismatches)

Seqs with only an unexpected site..... 2

Seqs with both expected and unexpected.... 2

Seqs with no sites..... 686

C: HpyCH4III, Bst4CI, or Taal in HC

In scoring whether the RE site of interest is present, only ONS that have 4 or fewer mismatches are counted.

Number of sequences.....		1617						acngt		acngt	
Id	Ntot	0	1	2	3	4	5	6	7	8	Ncut
1	244	78	92	43	18	10	1	2	0	0	241
2	457	69	150	115	66	34	11	8	3	1	434
3	173	52	45	36	22	14	3	0	0	1	169
4	16	0	3	2	2	1	6	0	1	1	124#5,1
5	4	0	0	1	0	1	1	0	1	0	145#6
6	15	1	0	1	0	6	4	1	1	1	158#8
7	23	4	8	5	2	2	1	1	0	0	21
8	9	1	1	1	0	3	2	1	0	0	6
9	7	1	3	1	1	0	0	1	0	0	6
10	23	7	3	5	5	2	1	0	0	0	22
11	35	5	10	7	6	3	3	0	1	0	31
12	18	2	3	2	2	6	1	0	2	0	15
13	3	1	2	0	0	0	0	0	0	0	3
14	117	29	23	28	22	8	4	2	1	0	110
15	75	21	25	13	9	1	4	2	0	0	69
16	14	2	2	2	3	0	3	1	1	0	9
17	2	0	0	1	0	0	1	0	0	0	1
18	1	0	0	1	0	0	0	0	0	0	1
19	2	0	0	0	0	0	0	0	0	2	0
20	34	4	9	9	4	5	3	0	0	0	31
21	17	5	4	2	2	3	1	0	0	0	16
22	75	15	17	24	7	10	1	1	0	0	73
23	40	14	15	4	5	1	0	1	0	0	39
24	213	26	56	60	42	20	7	2	0	0	204
Group	337	471	363	218	130	58	23	11	6	(SEQ ID NOS 192-215, respectively	

Cumulative	337	808	1171	1389	1519	1577	1600	1611	1617
Seqs with the expected RE site only.....	1511								
Seqs with only an unexpected site.....	0								
Seqs with both expected and unexpected.....	8								
Seqs with no sites.....	0								

in order of appearance)

Please delete Table 5D and replace it with the following table:

Table 5D:

Analysis repeated using only 8 best REadaptors

Id	Ntot	0	1	2	3	4	5	6	7	8+				
1	301	78	101	54	32	16	9	10	1	0	281	102#1		
ccgtgtattactgtgcgagaga <u>(SEQ ID NO: 267)</u>														
2	493	69	155	125	73	37	14	11	3	6	459	103#2		
ctgtgtattactgtgcgagaga <u>(SEQ ID NO: 268)</u>														
3	189	52	45	38	23	18	5	4	1	3	176	108#3		
ccgtgtattactgtgcgagagg <u>(SEQ ID NO: 269)</u>														
4	127	29	23	28	24	10	6	5	2	0	114	323#22		
ccgtatattactgtgcgaaaga <u>(SEQ ID NO: 270)</u>														
5	78	21	25	14	11	1	4	2	0	0	72	330#23		
ctgtgtattactgtgcgaaaga 6 79 15 17 25 8 11 1 2 0 0														
76	439#44	ctgtgtattactgtgcgagaca <u>(SEQ ID NO: 272)</u>												
7	43	14	15	5	5	3	0	1	0	0	42	551#48		
ccatgtattactgtgcgagaca <u>(SEQ ID NO: 273)</u>														
8	307	26	63	72	51	38	24	14	13	6	250	5a#49		
ccatgtattactgtgcgaga <u>(residues 1-20 of SEQ ID NO: 274)</u>														
1	102#1	ccgtgtattactgtgcgagaga											ccgtgtattactgtgcgagaga	
2	103#2	ctgtgtattactgtgcgagaga											.t.....	
3	108#3	ccgtgtattactgtgcgagagg										g	
4	323#22	ccgtatattactgtgcgaaaga										a.....a...	
5	330#23	ctgtgtattactgtgcgaaaga											.t.....a...	
6	439#44	ctgtgtattactgtgcgagaca											.t.....c.	
7	551#48	ccatgtattactgtgcgagaca											..a.....c.	
8	5a#49	ccatgtattactgtgcgagaAA											..a.....AA	
<u>(SEQ ID NOS 267-274, respectively in order of appearance)</u>														
Seqs with the expected RE site only..... 1463 / 1617														
Seqs with only an unexpected site..... 0														
Seqs with both expected and unexpected.... 7														
Seqs with no sites..... 0														

Please delete Table 6 and replace it with the following table:

Table 6: Human HC GLG FR1 Sequences

VH Exon - Nucleotide sequence alignment

VH1

1-02 CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGA TAC ACC TTC ACC (SEQ ID NO: 216)
1-03 cag gtC cag ctT gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag gct tct gga tac acc ttc acT (SEQ ID NO: 217)
1-08 cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc (SEQ ID NO: 218)
1-18 cag gtT cag ctg gtg cag tct ggA gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct ggT tac acc ttT acc (SEQ ID NO: 219)
1-24 cag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gTt tcC gga tac acc Ctc acT (SEQ ID NO: 220)
1-45 cag Atg cag ctg gtg cag tct ggg gct gag gtg aag aag Act ggg Tcc tca gtg aag gtT tcc tgc aag gct tcC gga tac acc ttc acc (SEQ ID NO: 221)
1-46 cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag gtT tcc tgc aag goA tct gga tac acc ttc acc (SEQ ID NO: 222)
1-58 caA Atg cag ctg gtg cag tct ggg Cct gag gtg aag aag cct ggg Acc tca gtg aag gtc tcc tgc aag gct tct gga tTc acc ttT acT (SEQ ID NO: 223)
1-69 cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tcG gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc (SEQ ID NO: 224)
1-e cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Tcc tcG gtg aag gtc tcc tgc aag gct tct gga GGc acc ttc aGc (SEQ ID NO: 225)
1-f Gag gtC cag ctg gtA cag tct ggg gct gag gtg aag aag cct ggg gcT Aca gtg aaA Atc tcc tgc aag gTt tct gga tac acc ttc acc (SEQ ID NO: 226)

VH2

2-05 CAG ATC ACC TTG AAG GAG TCT GGT CCT ACG CTG GTG AAA CCC ACA CAG ACC CTC ACG CTG ACC TGC ACC TTC TCT GGG TTC TCA CTC AGC (SEQ ID NO: 227)
2-26 cag Gtc acc ttg aag gag tct ggt cct GTg ctg gtg aaa ccc aca Gag acc ctc acg ctg acc tgc acc Gtc tct ggg ttc tca ctc agc (SEQ ID NO: 228)
2-70 cag Gtc acc ttg aag gag tct ggt cct Gcg ctg gtg aaa ccc aca cag acc ctc acA ctg acc tgc acc ttc tct ggg ttc tca ctc agc (SEQ ID NO: 229)

VH3

3-07 GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGT (SEQ ID NO: 230)
3-09 gaA gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggC Agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt Gat (SEQ ID NO: 231)
3-11 Cag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc Aag cct ggA ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 232)
3-13 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 233)

3-15 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA Aag cct ggg ggg tcc ctT aga
 ctc tcc tgt gca gcc tct gga ttc acT ttC agt (SEQ ID NO: 234)
 3-20 gag gtg cag ctg gtg gag tct ggg gga ggT Gtg gtA cGg cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttt Gat (SEQ ID NO: 235)
 3-21 gag gtg cag ctg gtg gag tct ggg gga ggc Ctg gtc Aag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 236)
 3-23 gag gtg cag ctg Ttg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttt agC (SEQ ID NO: 237)
 3-30 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 238)
 3-30.3 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 239)
 3-30.5 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 240)
 3-33 Cag gtg cag ctg gtg gag tct ggg gga ggc Gtg gtc cag cct ggg Agg tcc ctg aga
 ctc tcc tgt gca gcG tct gga ttc acc ttC agt (SEQ ID NO: 241)
 3-43 gaA gtg cag ctg gtg gag tct ggg gga gTc Gtg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttt Gat (SEQ ID NO: 242)
 3-48 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 243)
 3-49 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtA cag ccA ggg Cgg tcc ctg aga
 ctc tcc tgt Aca gcT tct gga ttc acc ttt Ggt (SEQ ID NO: 244)
 3-53 gag gtg cag ctg gtg gag Act ggA gga ggc ttg Atc cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct ggG ttc acc GtC agt (SEQ ID NO: 245)
 3-64 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 246)
 3-66 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc GtC agt (SEQ ID NO: 247)
 3-72 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggA ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 248)
 3-73 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg tcc ctg aAa
 ctc tcc tgt gca gcc tct ggG ttc acc ttC agt (SEQ ID NO: 249)
 3-74 gag gtg cag ctg gtg gag tcC ggg gga ggc ttA gtT cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc ttC agt (SEQ ID NO: 250)
 3-d gag gtg cag ctg gtg gag tct Cgg gga gTc ttg gtA cag cct ggg ggg tcc ctg aga
 ctc tcc tgt gca gcc tct gga ttc acc GtC agt (SEQ ID NO: 251)
 VH4
 4-04 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GGG ACC CTG TCC
 CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC AGC (SEQ ID NO: 252)
 4-28 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAC acc ctg tcc
 ctc acc tgc gct gtc tct ggt TAc tcc atc agc (SEQ ID NO: 253)
 4-30.1 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc
 ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 254)

4-30.2 cag Ctg cag ctg cag gag tcC ggc Tca gga ctg gtg aag cct tcA CAg acc ctg tcc
ctc acc tgc gct gtc tct ggt ggc tcc atc agc (SEQ ID NO: 255)

4-30.4 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 256)

4-31 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcA CAg acc ctg tcc
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 257)

4-34 cag gtg cag ctA cag Cag tGg ggc Gca gga ctg Ttg aag cct tcg gAg acc ctg tcc
ctc acc tgc gct gtc tAt ggt ggG tcc Ttc agT (SEQ ID NO: 258)

4-39 cag Ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
ctc acc tgc Act gtc tct ggt ggc tcc atc agc (SEQ ID NO: 259)

4-59 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
ctc acc tgc Act gtc tct ggt ggc tcc atc agT (SEQ ID NO: 260)

4-61 cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
ctc acc tgc Act gtc tct ggt ggc tcc Gtc agc (SEQ ID NO: 261)

4-b cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gAg acc ctg tcc
ctc acc tgc gct gtc tct ggt TAc tcc atc agc (SEQ ID NO: 262)

VH5

5-51 GAG GTG CAG CTG GTG CAG TCT GGA GCA GAG GTG AAA AAG CCC GGG GAG TCT CTG AAG
ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC (SEQ ID NO: 263)

5-a gaA gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc ggg gag tct ctg aGg
atc tcc tgt aag ggt tct gga tac agc ttt acc (SEQ ID NO: 264)

VH6

6-1 CAG GTA CAG CTG CAG CAG TCA GGT CCA GGA CTG GTG AAG CCC TCG CAG ACC CTC TCA
CTC ACC TGT GCC ATC TCC GGG GAC AGT GTC TCT (SEQ ID NO: 265)

VH7

7-4.1 CAG GTG CAG CTG GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG
GTT TCC TGC AAG GCT TCT GGA TAC ACC TTC ACT (SEQ ID NO: 266)

Please delete Table 7 and replace it with the following table:

Table 7: RERS sites in Human HC GLG FR1s where there are at least 20 GLGs cut

BsgI GTGCAG						71 (cuts 16/14 bases to right)	
1: 4	1: 13	2: 13	3: 4	3: 13	4: 13		
6: 13	7: 4	7: 13	8: 13	9: 4	9: 13		
10: 4	10: 13	15: 4	15: 65	16: 4	16: 65		
17: 4	17: 65	18: 4	18: 65	19: 4	19: 65		
20: 4	20: 65	21: 4	21: 65	22: 4	22: 65		
23: 4	23: 65	24: 4	24: 65	25: 4	25: 65		
26: 4	26: 65	27: 4	27: 65	28: 4	28: 65		
29: 4	30: 4	30: 65	31: 4	31: 65	32: 4		
32: 65	33: 4	33: 65	34: 4	34: 65	35: 4		
35: 65	36: 4	36: 65	37: 4	38: 4	39: 4		
41: 4	42: 4	43: 4	45: 4	46: 4	47: 4		
48: 4	48: 13	49: 4	49: 13	51: 4			

There are 39 hits at base# 4

There are 21 hits at base# 65

-"-	ctgcac	9
12: 63	13: 63	14: 63
44: 63	45: 63	46: 63

BbvI GCAGC						
65						
1: 6	3: 6	6: 6	7: 6	8: 6	9: 6	
10: 6	15: 6	15: 67	16: 6	16: 67	17: 6	
17: 67	18: 6	18: 67	19: 6	19: 67	20: 6	
20: 67	21: 6	21: 67	22: 6	22: 67	23: 6	
23: 67	24: 6	24: 67	25: 6	25: 67	26: 6	
26: 67	27: 6	27: 67	28: 6	28: 67	29: 6	
30: 6	30: 67	31: 6	31: 67	32: 6	32: 67	
33: 6	33: 67	34: 6	34: 67	35: 6	35: 67	
36: 6	36: 67	37: 6	38: 6	39: 6	40: 6	
41: 6	42: 6	43: 6	44: 6	45: 6	46: 6	
47: 6	48: 6	49: 6	50: 12	51: 6		

**There are 43 hits at base# 6 Bolded sites very near sit s
listed below**

There are 21 hits at base# 67

-"- gctgc 13
37: 9 38: 9 39: 9 40: 3 40: 9 41: 9
42: 9 44: 3 44: 9 45: 9 46: 9 47: 9
50: 9

There are 11 hits at base# 9

BsOfI GCngc 78
1: 6 3: 6 6: 6 7: 6 8: 6 9: 6
10: 6 15: 6 15: 67 16: 6 16: 67 17: 6
17: 67 18: 6 18: 67 19: 6 19: 67 20: 6
20: 67 21: 6 21: 67 22: 6 22: 67 23: 6
23: 67 24: 6 24: 67 25: 6 25: 67 26: 6
26: 67 27: 6 27: 67 28: 6 28: 67 29: 6
30: 6 30: 67 31: 6 31: 67 32: 6 32: 67
33: 6 33: 67 34: 6 34: 67 35: 6 35: 67
36: 6 36: 67 37: 6 37: 9 38: 6 38: 9
39: 6 39: 9 40: 3 40: 6 40: 9 41: 6
41: 9 42: 6 42: 9 43: 6 44: 3 44: 6
44: 9 45: 6 45: 9 46: 6 46: 9 47: 6
47: 9 48: 6 49: 6 50: 9 50: 12 51: 6

There are 43 hits at base# 6 These often occur together.

There are 11 hits at base# 9

There are 2 hits at base# 3

There are 21 hits at base# 67

TseI Gcwgc 78
1: 6 3: 6 6: 6 7: 6 8: 6 9: 6
10: 6 15: 6 15: 67 16: 6 16: 67 17: 6
17: 67 18: 6 18: 67 19: 6 19: 67 20: 6
20: 67 21: 6 21: 67 22: 6 22: 67 23: 6
23: 67 24: 6 24: 67 25: 6 25: 67 26: 6
26: 67 27: 6 27: 67 28: 6 28: 67 29: 6
30: 6 30: 67 31: 6 31: 67 32: 6 32: 67
33: 6 33: 67 34: 6 34: 67 35: 6 35: 67
36: 6 36: 67 37: 6 37: 9 38: 6 38: 9

<u>39:</u>	6	<u>39:</u>	9	<u>40:</u>	3	<u>40:</u>	6	<u>40:</u>	9	<u>41:</u>	6
<u>41:</u>	9	<u>42:</u>	6	<u>42:</u>	9	<u>43:</u>	6	<u>44:</u>	3	<u>44:</u>	6
<u>44:</u>	9	<u>45:</u>	6	<u>45:</u>	9	<u>46:</u>	6	<u>46:</u>	9	<u>47:</u>	6
<u>47:</u>	9	<u>48:</u>	6	<u>49:</u>	6	<u>50:</u>	9	<u>50:</u>	12	<u>51:</u>	6

There are 43 hits at base# 6 Often together.

There are 11 hits at base# 9

There are 2 hits at base# 3

There are 1 hits at base# 12

There are 21 hits at base# 67

MspAII CMGckg											
48											
1:	7	3:	7	4:	7	5:	7	6:	7	7:	7
8:	7	9:	7	10:	7	11:	7	15:	7	16:	7
17:	7	18:	7	19:	7	20:	7	21:	7	22:	7
23:	7	24:	7	25:	7	26:	7	27:	7	28:	7
29:	7	30:	7	31:	7	32:	7	33:	7	34:	7
35:	7	36:	7	37:	7	38:	7	39:	7	<u>40:</u>	1
<u>40:</u>	7	41:	7	42:	7	<u>44:</u>	1	<u>44:</u>	7	45:	7
46:	7	47:	7	48:	7	49:	7	50:	7	51:	7

There are 46 hits at base# 7

PvuII CAGctg											
48											
1:	7	3:	7	4:	7	5:	7	6:	7	7:	7
8:	7	9:	7	10:	7	11:	7	15:	7	16:	7
17:	7	18:	7	19:	7	20:	7	21:	7	22:	7
23:	7	24:	7	25:	7	26:	7	27:	7	28:	7
29:	7	30:	7	31:	7	32:	7	33:	7	34:	7
35:	7	36:	7	37:	7	38:	7	39:	7	<u>40:</u>	1
<u>40:</u>	7	41:	7	42:	7	<u>44:</u>	1	<u>44:</u>	7	45:	7
46:	7	47:	7	48:	7	49:	7	50:	7	51:	7

There are 46 hits at base# 7

There are 2 hits at base# 1

AluI AGct											
54											
1:	8	2:	8	3:	8	4:	8	4:	24	5:	8

6:	8	7:	8	8:	8	9:	8	10:	8	11:	8
15:	8	16:	8	17:	8	18:	8	19:	8	20:	8
21:	8	22:	8	23:	8	24:	8	25:	8	26:	8
27:	8	28:	8	29:	8	29:	69	30:	8	31:	8
32:	8	33:	8	34:	8	35:	8	36:	8	37:	8
38:	8	39:	8	40:	2	40:	8	41:	8	42:	8
43:	8	44:	2	44:	8	45:	8	46:	8	47:	8
48:	8	48:	82	49:	8	49:	82	50:	8	51:	8

There are 48 hits at base# 8

There are 2 hits at base# 2

DdeI	Ctnag		48		
1:	26	1:	48	2:	26
4:	26	4:	48	5:	26
7:	26	7:	48	8:	26
11:	26	12:	85	13:	85
17:	52	18:	52	19:	52
23:	52	24:	52	25:	52
29:	52	30:	52	31:	52
35:	52	36:	52	40:	24

There are 22 hits at base# 52 52 and 48 never together.

There are 9 hits at base# 48

There are 12 hits at base# 26 26 and 24 never together.

HphI	tcacc		42		
1:	86	3:	86	6:	86
12:	5	13:	5	14:	5
18:	80	20:	80	21:	80
25:	80	26:	80	27:	80
31:	80	32:	80	33:	80
37:	59	38:	59	39:	59
43:	59	44:	59	45:	59

There are 22 hits at base# 80 80 and 86 never together

There are 5 hits at base# 86

There are 12 hits at base# 59

BssKI Nccnngg		50					
1: 39	2: 39	3: 39	4: 39	5: 39	7: 39		
8: 39	9: 39	10: 39	11: 39	15: 39	16: 39		
17: 39	18: 39	19: 39	20: 39	21: 29	21: 39		
22: 39	23: 39	24: 39	25: 39	26: 39	27: 39		
28: 39	29: 39	30: 39	31: 39	32: 39	33: 39		
34: 39	35: 19	35: 39	36: 39	37: 24	38: 24		
39: 24	41: 24	42: 24	44: 24	45: 24	46: 24		
47: 24	<u>48: 39</u>	<u>48: 40</u>	<u>49: 39</u>	<u>49: 40</u>	50: 24		
50: 73	51: 39						

There are 35 hits at base# 39 39 and 40 together twice.

There are 2 hits at base# 40

BsaJI Ccnngg		47					
1: 40	2: 40	3: 40	4: 40	5: 40	7: 40		
8: 40	9: 40	9: 47	10: 40	10: 47	11: 40		
15: 40	18: 40	19: 40	20: 40	21: 40	22: 40		
23: 40	24: 40	25: 40	26: 40	27: 40	28: 40		
29: 40	30: 40	31: 40	32: 40	34: 40	35: 20		
35: 40	36: 40	37: 24	38: 24	39: 24	41: 24		
42: 24	44: 24	45: 24	46: 24	47: 24	<u>48: 40</u>		
<u>48: 41</u>	<u>49: 40</u>	<u>49: 41</u>	50: 74	51: 40			

There are 32 hits at base# 40 40 and 41 together twice

There are 2 hits at base# 41

There are 9 hits at base# 24

There are 2 hits at base# 47

BstNI CCwgg		44					
PspGI ccwgg							
ScrFI (\$M.HpaII) CCwgg							
1: 40	2: 40	3: 40	4: 40	5: 40	7: 40		
8: 40	9: 40	10: 40	11: 40	15: 40	16: 40		
17: 40	18: 40	19: 40	20: 40	21: 30	21: 40		
22: 40	23: 40	24: 40	25: 40	26: 40	27: 40		
28: 40	29: 40	30: 40	31: 40	32: 40	33: 40		

34: 40	35: 40	36: 40	37: 25	38: 25	39: 25
41: 25	42: 25	44: 25	45: 25	46: 25	47: 25
50: 25	51: 40				

There are 33 hits at base# 40

ScrFI CCnngg			50		
1: 40	2: 40	3: 40	4: 40	5: 40	7: 40
8: 40	9: 40	10: 40	11: 40	15: 40	16: 40
17: 40	18: 40	19: 40	20: 40	21: 30	21: 40
22: 40	23: 40	24: 40	25: 40	26: 40	27: 40
28: 40	29: 40	30: 40	31: 40	32: 40	33: 40
34: 40	35: 20	35: 40	36: 40	37: 25	38: 25
39: 25	41: 25	42: 25	44: 25	45: 25	46: 25
47: 25	48: 40	48: 41	49: 40	49: 41	50: 25
50: 74	51: 40				

There are 35 hits at base# 40

There are 2 hits at base# 41

EcoO109I RGgnccy			34		
1: 43	2: 43	3: 43	4: 43	5: 43	6: 43
7: 43	8: 43	9: 43	10: 43	15: 46	16: 46
17: 46	18: 46	19: 46	20: 46	21: 46	22: 46
23: 46	24: 46	25: 46	26: 46	27: 46	28: 46
30: 46	31: 46	32: 46	33: 46	34: 46	35: 46
36: 46	37: 46	43: 79	51: 43		

There are 22 hits at base# 46 46 and 43 never together

There are 11 hits at base# 43

NlaIV GGNncc			71		
1: 43	2: 43	3: 43	4: 43	5: 43	6: 43
7: 43	8: 43	9: 43	9: 79	10: 43	10: 79
<u>15: 46</u>	<u>15: 47</u>	16: 47	<u>17: 46</u>	<u>17: 47</u>	<u>18: 46</u>
<u>18: 47</u>	<u>19: 46</u>	<u>19: 47</u>	<u>20: 46</u>	<u>20: 47</u>	<u>21: 46</u>
<u>21: 47</u>	<u>22: 46</u>	<u>22: 47</u>	23: 47	24: 47	25: 47
<u>26: 47</u>	<u>27: 46</u>	<u>27: 47</u>	<u>28: 46</u>	<u>28: 47</u>	29: 47
<u>30: 46</u>	<u>30: 47</u>	<u>31: 46</u>	<u>31: 47</u>	<u>32: 46</u>	<u>32: 47</u>

<u>33: 46</u>	<u>33: 47</u>	<u>34: 46</u>	<u>34: 47</u>	<u>35: 46</u>	<u>35: 47</u>
<u>36: 46</u>	<u>36: 47</u>	<u>37: 21</u>	<u>37: 46</u>	<u>37: 47</u>	<u>37: 79</u>
38: 21	39: 21	39: 79	40: 79	41: 21	41: 79
42: 21	42: 79	43: 79	44: 21	44: 79	45: 21
45: 79	46: 21	46: 79	47: 21	51: 43	

There are 23 hits at base# 47 46 & 47 often together

There are 17 hits at base# 46 There are 11 hits at base# 43

Sau96I Ggncc								
70								
1: 44	2: 3	2: 44	3: 44	4: 44	5: 3	5: 44	6:	
44								
7: 44	8: 22	8: 44	9: 44	10: 44	11: 3	12: 22	13:	
22								
14: 22	15: 33	15: 47	16: 47	17: 47	18: 47	19: 47	20:	
47								
21: 47	22: 47	23: 33	23: 47	24: 33	24: 47	25: 33	25:	
47								
26: 33	26: 47	27: 47	28: 47	29: 47	30: 47	31: 33	31:	
47								
32: 33	32: 47	33: 33	33: 47	34: 33	34: 47	35: 47	36:	
47								
<u>37: 21</u>	<u>37: 22</u>	37: 47	<u>38: 21</u>	<u>38: 22</u>	39: 21	39: 22	41:	
21								
41: 22	42: 21	42: 22	43: 80	44: 21	44: 22	45: 21	45:	
22								
46: 21	46: 22	47: 21	47: 22	50: 22	51: 44			

There are 23 hits at base# 47 These do not occur together.

There are 11 hits at base# 44

There are 14 hits at base# 22 These do occur together.

There are 9 hits at base# 21

(SEQ ID NO: 13)

BsmAI GTCTCNnnnn 22

1: 58	3: 58	4: 58	5: 58	8: 58	9: 58
10: 58	13: 70	36: 18	37: 70	38: 70	39: 70
40: 70	41: 70	42: 70	44: 70	45: 70	46: 70
47: 70	48: 48	49: 48	50: 85		

There are 11 hits at base# 70

(SEQ ID NO: 14)

-"- Nnnnnnngagac 27

13: 40	15: 48	16: 48	17: 48	18: 48	20: 48
21: 48	22: 48	23: 48	24: 48	25: 48	26: 48
27: 48	28: 48	29: 48	30: 10	30: 48	31: 48
32: 48	33: 48	35: 48	36: 48	43: 40	44: 40
45: 40	46: 40	47: 40			

There are 20 hits at base# 48

AvaII Ggwcc 44

Sau96I (\$M.HaeIII) Ggwcc 44

2: 3	5: 3	6: 44	8: 44	9: 44	10: 44
11: 3	12: 22	13: 22	14: 22	15: 33	15: 47
16: 47	17: 47	18: 47	19: 47	20: 47	21: 47
22: 47	23: 33	23: 47	24: 33	24: 47	25: 33
25: 47	26: 33	26: 47	27: 47	28: 47	29: 47
30: 47	31: 33	31: 47	32: 33	32: 47	33: 33
33: 47	34: 33	34: 47	35: 47	36: 47	37: 47
43: 80	50: 22				

There are 23 hits at base# 47 44 & 47 never together

There are 4 hits at base# 44

PpuMI RGgwccy 27

6: 43	8: 43	9: 43	10: 43	15: 46	16: 46
17: 46	18: 46	19: 46	20: 46	21: 46	22: 46
23: 46	24: 46	25: 46	26: 46	27: 46	28: 46
30: 46	31: 46	32: 46	33: 46	34: 46	35: 46
36: 46	37: 46	43: 79			

There are 22 hits at base# 46 43 and 46 never occur together.

There are 4 hits at base# 43

BsmFI GGGAC

3

8: 43	37: 46	50: 77				
-"- gtccc			33			
15: 48	16: 48	17: 48	1: 0	1: 0	20: 48	
21: 48	22: 48	23: 48	24: 48	25: 48	26: 48	
27: 48	28: 48	29: 48	30: 48	31: 48	32: 48	
33: 48	34: 48	35: 48	36: 48	37: 54	38: 54	
39: 54	40: 54	41: 54	42: 54	43: 54	44: 54	
45: 54	46: 54	47: 54				

There are 20 hits at base# 48

There are 11 hits at base# 54

HinfI Gantc

80

8: 77	12: 16	13: 16	14: 16	15: 16	15: 56	
15: 77	16: 16	16: 56	16: 77	17: 16	17: 56	
17: 77	18: 16	18: 56	18: 77	19: 16	19: 56	
19: 77	20: 16	20: 56	20: 77	21: 16	21: 56	
21: 77	22: 16	22: 56	22: 77	23: 16	23: 56	
23: 77	24: 16	24: 56	24: 77	25: 16	25: 56	
25: 77	26: 16	26: 56	26: 77	27: 16	27: 26	
27: 56	27: 77	28: 16	28: 56	28: 77	29: 16	
29: 56	29: 77	30: 56	31: 16	31: 56	31: 77	
32: 16	32: 56	32: 77	33: 16	33: 56	33: 77	
34: 16	35: 16	35: 56	35: 77	36: 16	36: 26	
36: 56	36: 77	37: 16	38: 16	39: 16	40: 16	
41: 16	42: 16	44: 16	45: 16	46: 16	47: 16	
48: 46	49: 46					

There are 34 hits at base# 16

TfiI Gawtc

21

8: 77	15: 77	16: 77	17: 77	18: 77	19: 77	
20: 77	21: 77	22: 77	23: 77	24: 77	25: 77	

26: 77 27: 77 28: 77 29: 77 31: 77 32: 77
33: 77 35: 77 36: 77

There are 21 hits at base# 77

MlyI GAGTC			38		
12: 16	13: 16	14: 16	15: 16	16: 16	17: 16
18: 16	19: 16	20: 16	21: 16	22: 16	23: 16
24: 16	25: 16	26: 16	27: 16	27: 26	28: 16
29: 16	31: 16	32: 16	33: 16	34: 16	35: 16
36: 16	36: 26	37: 16	38: 16	39: 16	40: 16
41: 16	42: 16	44: 16	45: 16	46: 16	47: 16
48: 46	49: 46				

There are 34 hits at base# 16

- " - GACTC 21
15: 56 16: 56 17: 56 18: 56 19: 56 20: 56
21: 56 22: 56 23: 56 24: 56 25: 56 26: 56
27: 56 28: 56 29: 56 30: 56 31: 56 32: 56
33: 56 35: 56 36: 56

There are 21 hits at base# 56

PleI gagtc		38					
12:	16	13:	16	14:	16	15:	16
18:	16	19:	16	20:	16	21:	16
24:	16	25:	16	26:	16	27:	16
27:	16	28:	16	29:	16	30:	16
31:	16	32:	16	33:	16	34:	16
35:	16	36:	26	37:	16	38:	16
39:	16	40:	16	41:	16	42:	16
43:	16	44:	16	45:	16	46:	16
47:	16	48:	46	49:	46		

There are 34 hits at base# 16

-"-" gactc 21
15: 56 16: 56 17: 56 18: 56 19: 56 20: 56
21: 56 22: 56 23: 56 24: 56 25: 56 26: 56
27: 56 28: 56 29: 56 30: 56 31: 56 32: 56
33: 56 35: 56 36: 56

There are 21 hits at base# 56

AlwNI CAGNNNctg 26
 15: 68 16: 68 17: 68 18: 68 19: 68 20: 68
 21: 68 22: 68 23: 68 24: 68 25: 68 26: 68
 27: 68 28: 68 29: 68 30: 68 31: 68 32: 68
 33: 68 34: 68 35: 68 36: 68 39: 46 40: 46
 41: 46 42: 46

There are 22 hits at base# 68

Please delete Table 8 and replace it with the following table:

Table 8: Kappa FR1 GLGs

! 1	2	3	4	5	6	7	8	9	10	11	12
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
! 13	14	15	16	17	18	19	20	21	22	23	
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! O12(<u>SEQ ID NO: 275</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! O2(<u>SEQ ID NO: 276</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! O18(<u>SEQ ID NO: 277</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! O8(<u>SEQ ID NO: 278</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! A20(<u>SEQ ID NO: 279</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! A30(<u>SEQ ID NO: 280</u>)
AAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCT	GCC	ATG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	! L14(<u>SEQ ID NO: 281</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	! L1(<u>SEQ ID NO: 282</u>)
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGT	! L15(<u>SEQ ID NO: 283</u>)
GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT
GCA	TCT	GTA	GGA	GAC	AGA	GTC	ACC	ATC	ACT	TGC	! L4(<u>SEQ ID NO: 284</u>)
GCC	ATC	CAG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT

GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L18 (SEQ ID NO: 285)
GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC GTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT ! L5 (SEQ ID NO: 286)
GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC GTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT ! L19 (SEQ ID NO: 287)
GAC ATC CAG TTG ACC CAG TCT CCA TCC TTC CTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L8 (SEQ ID NO: 288)
GCC ATC CGG ATG ACC CAG TCT CCA TTC TCC CTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L23 (SEQ ID NO: 289)
GCC ATC CGG ATG ACC CAG TCT CCA TCC TCA TTC TCT
GCA TCT ACA GGA GAC AGA GTC ACC ATC ACT TGT ! L9 (SEQ ID NO: 290)
GTC ATC TGG ATG ACC CAG TCT CCA TCC TTA CTC TCT
GCA TCT ACA GGA GAC AGA GTC ACC ATC AGT TGT ! L24 (SEQ ID NO: 291)
GCC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L11 (SEQ ID NO: 292)
GAC ATC CAG ATG ACC CAG TCT CCT TCC ACC CTG TCT
GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC ! L12 (SEQ ID NO: 293)
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! O11 (SEQ ID NO: 294)
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC CTG CCC
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! O1 (SEQ ID NO: 295)
GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A17 (SEQ ID NO: 296)
GAT GTT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A1 (SEQ ID NO: 297)
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC
GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC ! A18 (SEQ ID NO: 298)
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCT CTG TCC
GTC ACC CCT GGA CAG CCG GCC TCC ATC TCC TGC ! A2 (SEQ ID NO: 299)
GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! A19 (SEQ ID NO: 300)
GAT ATT GTG ATG ACT CAG TCT CCA CTC TCC CTG CCC
GTC ACC CCT GGA GAG CCG GCC TCC ATC TCC TGC ! A3 (SEQ ID NO: 301)
GAT ATT GTG ATG ACC CAG ACT CCA CTC TCC TCA CCT
GTC ACC CTT GGA CAG CCG GCC TCC ATC TCC TGC ! A23 (SEQ ID NO: 302)

GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! A27 (SEQ ID NO: 303)
 GAA ATT GTG TTG ACG CAG TCT CCA GCC ACC CTG TCT
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! A11 (SEQ ID NO: 304)
 GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT
 GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L2 (SEQ ID NO: 305)
 GAA ATA GTG ATG ACG CAG TCT CCA GCC ACC CTG TCT
 GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L16 (SEQ ID NO: 306)
 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L6 (SEQ ID NO: 307)
 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L20 SEQ ID NO: 308)
 GAA ATT GTA ATG ACA CAG TCT CCA GCC ACC CTG TCT
 TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L25 (SEQ ID NO: 309)
 GAC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT
 GTG TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC ! B3 (SEQ ID NO: 310)
 GAA ACG ACA CTC ACG CAG TCT CCA GCA TTC ATG TCA
 GCG ACT CCA GGA GAC AAA GTC AAC ATC TCC TGC ! B2 (SEQ ID NO: 311)
 GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT
 GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC ! A26 (SEQ ID NO: 312)
 GAA ATT GTG CTG ACT CAG TCT CCA GAC TTT CAG TCT
 GTG ACT CCA AAG GAG AAA GTC ACC ATC ACC TGC ! A10 (SEQ ID NO: 313)
 GAT GTT GTG ATG ACA CAG TCT CCA GCT TTC CTC TCT
 GTG ACT CCA GGG GAG AAA GTC ACC ATC ACC TGC ! A14 (SEQ ID NO: 314)

Please delete Table 10 and replace it with the following table:

Table 10 Lambda FR1 GLG sequences

! VL1

CAG TCT GTG CTG ACT CAG CCA CCC TCG GTG TCT GAA
 GCC CCC AGG CAG AGG GTC ACC ATC TCC TGT ! 1a
(SEQ ID NO: 315)
 cag tct gtg ctg acG cag ccG ccc tcA gtg tct gGG
 gcc ccA Ggg cag agg gtc acc atc tcc tgC ! 1e

(SEQ ID NO: 316)

cag tct gtg ctg act cag cca ccc tcA gCg tct gGG
Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1c

(SEQ ID NO: 317)

cag tct gtg ctg act cag cca ccc tcA gCg tct gGG
Acc ccc Ggg cag agg gtc acc atc tcT tgt ! 1g

(SEQ ID NO: 318)

cag tct gtg Ttg acG cag ccG ccc tcA gtg tct gCG
gcc ccA GgA cag aAg gtc acc atc tcc tgC ! 1b

! VL2

(SEQ ID NO: 319)

CAG TCT GCC CTG ACT CAG CCT CCC TCC GCG TCC GGG
TCT CCT GGA CAG TCA GTC ACC ATC TCC TGC ! 2c

(SEQ ID NO: 320)

cag tct gcc ctg act cag cct cGc tcA gTg tcc ggg
tct cct gga cag tca gtc acc atc tcc tgc ! 2e

(SEQ ID NO: 321)

cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg
tct cct gga cag tcG Atc acc atc tcc tgc ! 2a2

(SEQ ID NO: 322)

cag tct gcc ctg act cag cct ccc tcc gTg tcc ggg
tct cct gga cag tca gtc acc atc tcc tgc ! 2d

(SEQ ID NO: 323)

cag tct gcc ctg act cag cct Gcc tcc gTg tcT ggg
tct cct gga cag tcG Atc acc atc tcc tgc ! 2b2

! VL3

(SEQ ID NO: 324)

TCC TAT GAG CTG ACT CAG CCA CCC TCA GTG TCC GTG
TCC CCA GGA CAG ACA GCC AGC ATC ACC TGC! 3r

(SEQ ID NO: 325)

tcc tat gag ctg act cag cca cTc tca gtg tcA gtg
Gcc cTG gga cag acG gcc agG atT acc tgT ! 3j

(SEQ ID NO: 326)

tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg
tcc cca gga caA acG gcc agG atc acc tgc! 3p

(SEQ ID NO: 327)

tcc tat gag ctg acA cag cca ccc tcG gtg tcA gtg
tcc cTa gga cag aTG gcc agG atc acc tgc ! 3a

(SEQ ID NO: 328)

tcT tCt gag ctg act cag GAC ccT GcT gtg tcT gtg
Gcc TTG gga cag aca gTc agG atc acA tgc ! 31

(SEQ ID NO: 329)

tcc tat gTg ctg act cag cca ccc tca gtg tcA gtg
Gcc cca gga Aag acG gcc agG atT acc tgT ! 3h

(SEQ ID NO: 330)

tcc tat gag ctg acA cag cTa ccc tcG gtg tcA gtg
tcc cca gga cag aca gcc agG atc acc tgc ! 3e

(SEQ ID NO: 331)

tcc tat gag ctg aTG cag cca ccc tcG gtg tcA gtg
tcc cca gga cag acG gcc agG atc acc tgc ! 3m

(SEQ ID NO: 332)

tcc tat gag ctg acA cag cca Tcc tca gtg tcA gtg
tcT ccG gga cag aca gcc agG atc acc tgc ! V2-19

! VL4

(SEQ ID NO: 333)

CTG CCT GTG CTG ACT CAG CCC CCG TCT GCA TCT GCC
TTG CTG GGA GCC TCG ATC AAG CTC ACC TGC ! 4c

(SEQ ID NO: 334)

cAg cct gtg ctg act caA TcA TcC tct gcC tct gcT
tCC ctg gga Tcc tcg Gtc aag ctc acc tgc ! 4a

(SEQ ID NO: 335)

cAg cTt gtg ctg act caA TcG ccC tct gcC tct gcc
tCC ctg gga gcc tcg Gtc aag ctc acc tgc ! 4b

! VL5

(SEQ ID NO: 336)

CAG CCT GTG CTG ACT CAG CCA CCT TCC TCC TCC GCA
TCT CCT GGA GAA TCC GCC AGA CTC ACC TGC ! 5e

(SEQ ID NO: 337)

cag Gct gtg ctg act cag ccG Gct tcc CTc tcT gca
tct cct gga gCa tcA gcc agT ctc acc tgc ! 5c

(SEQ ID NO: 338)

cag cct gtg ctg act cag cca Tct tcc CAT tcT gca
tct Tct gga gCa tcA gTc aga ctc acc tgc ! 5b

! VL6

(SEQ ID NO: 339)

AAT TTT ATG CTG ACT CAG CCC CAC TCT GTG TCG GAG
TCT CCG GGG AAG ACG GTA ACC ATC TCC TGC ! 6a

! VL7 (SEQ ID NO: 340)
 CAG ACT GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG
 TCC CCA GGA GGG ACA GTC ACT CTC ACC TGT ! 7a
(SEQ ID NO: 341)
 cag Gct gtg gtg act cag gag ccc tca ctg act gtg
 tcc cca gga ggg aca gtc act ctc acc tgt ! 7b
! VL8 (SEQ ID NO: 342)
 CAG ACT GTG GTG ACC CAG GAG CCA TCG TTC TCA GTG
 TCC CCT GGA GGG ACA GTC ACA CTC ACT TGT ! 8a
! VL9 (SEQ ID NO: 343)
 CAG CCT GTG CTG ACT CAG CCA CCT TCT GCA TCA GCC
 TCC CTG GGA GCC TCG GTC ACA CTC ACC TGC ! 9a
! VL10 (SEQ ID NO: 344)
 CAG GCA GGG CTG ACT CAG CCA CCC TCG GTG TCC AAG
 GGC TTG AGA CAG ACC GCC ACA CTC ACC TGC ! 10a
(SEQ ID NO: 345)

Please delete Table 11 and replace it with the following table:

Table 11 RERSs found in human lambda FR1 GLGs

! There are 31 lambda GLGs

MlyI NnnnnnGACTC (SEQ ID NO: 346) 25

1:	6	3:	6	4:	6	6:	6	7:	6	8:	6
9:	6	10:	6	11:	6	12:	6	15:	6	16:	6
20:	6	21:	6	22:	6	23:	6	23:	50	24:	6
25:	6	25:	50	26:	6	27:	6	28:	6	30:	6
31:	6										

There are 23 hits at base# 6

-" - GAGTCNNNNn (SEQ ID NO: 347) 1

26: 34

MwoI GCNNNNNnngc (SEQ ID NO: 348) 20

1: 9	2: 9	3: 9	4: 9	11: 9	11: 56
12: 9	13: 9	14: 9	16: 9	17: 9	18: 9
19: 9	20: 9	23: 9	24: 9	25: 9	26: 9
30: 9	31: 9				

There are 19 hits at base# 9

HinfI Gantc		27			
1: 12	3: 12	4: 12	6: 12	7: 12	8: 12
9: 12	10: 12	11: 12	12: 12	15: 12	16: 12
20: 12	21: 12	22: 12	23: 12	23: 46	23: 56
24: 12	25: 12	25: 56	26: 12	26: 34	27: 12
28: 12	30: 12	31: 12			

There are 23 hits at base# 12

PleI gactc		25			
1: 12	3: 12	4: 12	6: 12	7: 12	8: 12
9: 12	10: 12	11: 12	12: 12	15: 12	16: 12
20: 12	21: 12	22: 12	23: 12	23: 56	24: 12
25: 12	25: 56	26: 12	27: 12	28: 12	30: 12
31: 12					

There are 23 hits at base# 12

-"- gagtc		1			
26: 34					

DdeI Ctnag		32			
1: 14	2: 24	3: 14	3: 24	4: 14	4: 24
5: 24	6: 14	7: 14	7: 24	8: 14	9: 14
10: 14	11: 14	11: 24	12: 14	12: 24	15: 5
15: 14	16: 14	16: 24	19: 24	20: 14	23: 14
24: 14	25: 14	26: 14	27: 14	28: 14	29: 30
30: 14	31: 14				

There are 21 hits at base# 14

BsaJI Ccnngg		38			
1: 23	1: 40	2: 39	2: 40	3: 39	3: 40
4: 39	4: 40	5: 39	11: 39	12: 38	12: 39
13: 23	13: 39	14: 23	14: 39	15: 38	16: 39

17: 23 17: 39 18: 23 18: 39 21: 38 21: 39
21: 47 22: 38 22: 39 22: 47 26: 40 27: 39
28: 39 29: 14 29: 39 30: 38 30: 39 30: 47
31: 23 31: 32

There are 17 hits at base# 39

There are 5 hits at base# 38

There are 5 hits at base# 40 Makes cleavage ragged.

MnI cctc 35
1: 23 2: 23 3: 23 4: 23 5: 23 6: 19
6: 23 7: 19 8: 23 9: 19 9: 23 10: 23
11: 23 13: 23 14: 23 16: 23 17: 23 18: 23
19: 23 20: 47 21: 23 21: 29 21: 47 22: 23
22: 29 22: 35 22: 47 23: 26 23: 29 24: 27
27: 23 28: 23 30: 35 30: 47 31: 23

There are 21 hits at base# 23

There are 3 hits at base# 19

There are 3 hits at base# 29

There are 1 hits at base# 26

There are 1 hits at base# 27 These could make cleavage ragged.

-" - gagg 7
1: 48 2: 48 3: 48 4: 48 27: 44 28: 44
29: 44

BssKI Nccngg 39
1: 40 2: 39 3: 39 3: 40 4: 39 4: 40
5: 39 6: 31 6: 39 7: 31 7: 39 8: 39
9: 31 9: 39 10: 39 11: 39 12: 38 12: 52
13: 39 13: 52 14: 52 16: 39 16: 52 17: 39
17: 52 18: 39 18: 52 19: 39 19: 52 21: 38
22: 38 23: 39 24: 39 26: 39 27: 39 28: 39
29: 14 29: 39 30: 38

There are 21 hits at base# 39

There are 4 hits at base# 38

There are 3 hits at base# 31

There are 3 hits at base# 40 Ragged

BstNI CCwgg

30

1: 41	2: 40	5: 40	6: 40	7: 40	8: 40
9: 40	10: 40	11: 40	12: 39	12: 53	13: 40
13: 53	14: 53	16: 40	16: 53	17: 40	17: 53
18: 40	18: 53	19: 53	21: 39	22: 39	23: 40
24: 40	27: 40	28: 40	29: 15	29: 40	30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

There are 4 hits at base# 39

There are 1 hits at base# 41 Ragged

PspGI ccwgg

30

1: 41	2: 40	5: 40	6: 40	7: 40	8: 40
9: 40	10: 40	11: 40	12: 39	12: 53	13: 40
13: 53	14: 53	16: 40	16: 53	17: 40	17: 53
18: 40	18: 53	19: 53	21: 39	22: 39	23: 40
24: 40	27: 40	28: 40	29: 15	29: 40	30: 39

There are 17 hits at base# 40

There are 7 hits at base# 53

There are 4 hits at base# 39

There are 1 hits at base# 41

ScrFI CCnigg

39

1: 41	2: 40	3: 40	3: 41	4: 40	4: 41
5: 40	6: 32	6: 40	7: 32	7: 40	8: 40
9: 32	9: 40	10: 40	11: 40	12: 39	12: 53
13: 40	13: 53	14: 53	16: 40	16: 53	17: 40
17: 53	18: 40	18: 53	19: 40	19: 53	21: 39
22: 39	23: 40	24: 40	26: 40	27: 40	28: 40
29: 15	29: 40	30: 39			

There are 21 hits at base# 40

There are 4 hits at base# 39

There are 3 hits at base# 41

MaeIII gtnac

16

1: 52 2: 52 3: 52 4: 52 5: 52 6: 52
7: 52 9: 52 26: 52 27: 10 27: 52 28: 10
28: 52 29: 10 29: 52 30: 52

There are 13 hits at base# 52

Tsp45I gtsac

15

1: 52 2: 52 3: 52 4: 52 5: 52 6: 52
7: 52 9: 52 27: 10 27: 52 28: 10 28: 52
29: 10 29: 52 30: 52

There are 12 hits at base# 52

HphI tcacc

26

1: 53 2: 53 3: 53 4: 53 5: 53 6: 53
7: 53 8: 53 9: 53 10: 53 11: 59 13: 59
14: 59 17: 59 18: 59 19: 59 20: 59 21: 59
22: 59 23: 59 24: 59 25: 59 27: 59 28: 59
30: 59 31: 59

There are 16 hits at base# 59

There are 10 hits at base# 53

BspMI ACCTGCNNNNn (SEQ ID NO: 349) 14

11: 61 13: 61 14: 61 17: 61 18: 61 19: 61
20: 61 21: 61 22: 61 23: 61 24: 61 25: 61
30: 61 31: 61

There are 14 hits at base# 61 Goes into CDR1

Please delete Table 13 and replace it with the following table:

Table 13

The following list of enzymes was taken from
<http://rebase.neb.com/cgi-bin/asymmlist>.

I have removed the enzymes that a) cut within the recognition, b) cut on both sides of the recognition, or c) have fewer than 2 bases between recognition and closest cut site.

REBASE Enzymes

04/13/2001

Type II restriction enzymes with asymmetric recognition sequences:

Enzymes	Recognition Sequence	Isoschizomers	Suppliers
AarI	CACCTGCNNNN^NNNN	-	Y
AceIII	CAGCTCNNNNNNN^NNNN	-	-
Bbr7I	GAAGACNNNNNNN^NNNN	-	-
BbvI	GCAGCBBBBBBBBB^NNNN	-	Y
BbvII	GAAGACNN^NNNN	-	-
Bce83I	CTTGAGNNNNNNNNNNNNN_NN^	-	-
BceAI	ACGGCBBBBBBBBB^NN	-	Y
BcefI	ACGGCBBBBBBBBB^N	-	-
BciVI	GTATCCNNNN_N^	BfuI	Y
BfiI	ACTGGGNNNN_N^	BmrI	Y
BinI	GGATCBBBBB^N	-	-
BscAI	GCATCBBBBB^NN	-	-
BseRI	GAGGAGNNNNNNNN_NN^	-	Y
BsmFI	GGGACBBBBBBBBB^NNNN	BspLU11III	Y
BspMI	ACCTGCNNNN^NNNN	Acc36I	Y
EciI	GGCGGAGNNNNNNNN_NN^	-	Y
Eco57I	CTGAAGNNNNNNNNNNNNNN_NN^	BspKT5I	Y
FauI	CCCGCBBBBB^NN	BstFZ438I	Y
FokI	GGATGNNNNNNNN^NNNN	BstPZ418I	Y
GsuI	CTGGAGNNNNNNNNNNNNNN_NN^	-	Y
HgaI	GACGCBBBBB^NNNN	-	Y
HphI	GGTGAGNNNNNN_N^	AsuHPI	Y
MboII	GAAGANNNNNN_N^	-	Y
MlyI	GAGTCBBBBB^	SchI	Y
MmeI	TCCRACBBBBBBBBBBBBBBBB_NN^	-	-
MnII	CCTCBBBBB_N^	-	Y
PleI	GAGTCBBBBB^N	PpsI	Y
RleAI	CCCACANNNNNNNNN_NNN^	-	-
SfaNI	GCATCBBBBB^NNNN	BspST5I	Y
SspD5I	GGTGAGNNNNNNN^	-	-
Sth132I	CCCGNNNN^NNNN	-	-
StsI	GGATGNNNNNNNNN^NNNN	-	-
TaqII	GACCGAGNNNNNNNN_NN^, CACCCAGNNNNNNNN_NN^	-	-
Tth11III	CAARCAGNNNNNNNN_NN^	-	-
UbaPI	CGAACG	-	-

(SEQ ID NOS 356-390, respectively in order of appearance)

The notation is [^] means cut the upper strand and means cut the lower strand. If the upper and lower strand are cut at the same place, then only [^] appears.

Please delete Table 14 and replace it with the following table:

Table 14
(FOKlact)

	5' - <u>cACATccGtg</u> TTGTT <u>cACGGATGtg</u> -3' (SEQ ID NO: 350)
(VHEX881)	5' -AATAGTAGAC TGCAGTGTCC TCAAGCCCTTA AGCTGTTCAT CTGCAAGTAG- AGAGTATTCT TAGAGTTCT TCTAGACTTA GTGAAAGCG-3' (SEQ ID NO: 351)
!	note that VHEX881 is the reverse complement of the ON below
!	[RC] 5' -cgCttcacTaag-
!	Scab.
!	Synthetic 3-23 as in Table 206
!	TCT AGA gac aac tct aag aat act ctc tac ttg cag atg -
XbaI..:	aac agc TTA AGG gct gag gac act GCA Gtc tac tat t-3' (SEQ ID NO: 352)
AfIII..:	
(VHBA881)	5' -cgCttcacTaag- TCT AGA gac aac tct aag aat act ctc tac ttg cag atg - aac agc TTA AGG gct gag gac act GCA Gtc tac tat t-3' (SEQ ID NO: 353)
(VHBB881)	5' -cgCttcacTaag- TCT AGA gac aac tct aag aat act ctc tac ttg cag atg - aac agc TTA AGG gct gag gac act GCA Gtc tac tat t-3' (SEQ ID NO: 354)
(VH881PCR)	5' -cgCttcacTaag TCT AGA gac aac -3' (SEQ ID NO: 355)

Please delete Table 15 and replace it with the following table:

Table 15: Use of *FokI* as "Universal Restriction Enzyme"

FokI - for dsDNA, | represents sites of cleavage

sites of cleavage

5' -cacGGATGtg--nnnnnnnn|nnnnnnnn-3' (SEQ ID NO:15)
 3' -gtgCCTACac--nnnnnnnnnnnn|nnn-5' (SEQ ID NO:16)
 RECOG
 NITion of *FokI*

Case I

5' - gtg|tatt-actgtgc..Substrate.....-3' (SEQ_ID_NO:17)
 3' - cac-ataa|tgacacg|
 5' - caCATCCqtq (SEQ_ID_NO:18)
 gtGTAGGcac\

Case II

5' - . . . gtgtatt|agac-tgc.. Substrate.....-3' (SEQ_ID_NO:19)
|cacataa-tctg|acg-5'
/gtgCCTAACac
\cacGGATGtg-3' (SEQ_ID_NO:20)

Case III (Case I rotated 180 degrees)

/gtgCCTAACac-5'
\cacGGATGtg
gtgtctt|acag-tcc-3' Adapter (SEQ ID NO:21)
3' - . . . cacagaa-tgtc|agg..substrate. . . . -5' (SEQ ID NO:22)

Case IV (Case II rotated 180 degrees)

3' - gtGTAGGcac\ (SEQ ID NO:23)
 5' - gag | tctc-actgagc
 Substrate 3' - ...ctc-agag | tgactcg...-5' (SEQ ID NO:24)

Improved *FokI* adapters

FokI - for dsDNA, | represents sites of cleavage

Case I
Stem 11, loop 5, stem 11, recognition 17

Please delete Table 16 and replace it with the following table:

Table 16 Human heavy chains bases 88.1 to 94.2

Number of sequences 840

Id	Ntot	Number of Mismatches.....						Name	Probe Sequence.....	Dot form.....
		0	1	2	3	4	5			
1	364	152	97	76	26	7	4	2	0	VHS881-1.1
2	265	150	60	33	13	5	4	0	0	VHS881-1.2
3	96	14	34	16	10	5	7	9	1	VHS881-2.1
4	20	0	3	4	9	2	2	0	0	VHS881-4.1
5	95	25	36	18	11	2	2	0	1	VHS881-9.1
840	341	230	147	69	21	19	11	2	(SEQ ID NOS 391-395, respectively in order of appearance)	
	341	571	718	787	808	827	838	840		

88 89 90 91 92 93 94 95 Codon number as in Table 195

Recognition..... Stem..... Loop. Stem.....
 (VHS881-1.1) 5'-gtctgtat tact-gtgcgag cACATccgtg TTGTT cAcggAT~~GT~~Tg-3'
 (VHS881-1.2) 5'-gccgtgtat tact-gtgcgag cACATccgtg TTGTT cAcggAT~~GT~~Tg-3'
 (VHS881-2.1) 5'-gccgtata tact-gtgcgag cACATccgtg TTGTT cAcggAT~~GT~~Tg-3'
 (VHS881-4.1) 5'-gccgtgtat tact-gtacgag cACATccgtg TTGTT cAcggAT~~GT~~Tg-3'
 (VHS881-9.1) 5'-gccccatgtat tact-gtgcgag cACATccgtg TTGTT cAcggAT~~GT~~Tg-3'

site of substrate cleavage

(Sequences in the left column above are SEQ ID NOS 391-395, respectively in order of appearance;
 sequences in the right column are all SEQ ID NO: 396)

(FOK1act) 5'-cAcATccgtg TTGTT cAcggATgtg-3' (SEQ ID NO: 396)

(VHEx881) 5'-ATAgTAgAc TgcAgTgTcc TcAgccCTTA AgcTgTcAT cTgcAAgTAG-
 AgAgTATTcT TAgAgTgTcTcTAgAcTTA gTgAAgg-3' (SEQ ID NO: 397)

! note that VHEx881 is the reverse complement of the ON below

[RC] 5'-cgCtccacTaag-
 Scab.....

Synthetic 3-23 as in Table 206
 | TCT | AGA | gac | aac | tct | aag | aat | act | ctc | tac | ttg | cag | atg | -

! XbaI...
! | aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|t-3'
! | AflII...
! |
! | (VHBA881) 5'-cgCttcacTaa^g
! | [TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
! | [aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgcg ag-3' (SEQ ID NO: 398)
! |
! | (VHBB881) 5'-cgCttcacTaa^g
! | [TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|-
! | [aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgcg ag-3' (SEQ ID NO: 618)
! |
! | (VH881PCR) 5'-cgCttcacTaa^g|TCT|AGA|gac|aac|3' (SEQ ID NO: 399)

Please delete Table 17 and replace it with the following table:

Table 17: Kappa, bases 12-30

ID	Ntot	0	1	2	3	4	5	6	Name	Sequence.....	Dot Form.....
1	84	40	21	20	1	2	0	0	SK12O12	gaccaggatccatccatcc (residues 26-44 of SEQ ID NO: 400)	
2	32	19	3	6	2	1	0	1	SK12A17	gactcgttccatcttc ...t.....ct.... (residues 26-44 of SEQ ID NO: 401)	
3	26	17	8	1	0	0	0	0	SK12A27	gacgagttccaggacc ...g.....gg.a. (residues 26-44 of SEQ ID NO: 402)	
4	40	21	18	1	0	0	0	0	SK12A11	gacgcgttccggccacc ...g.....g.a. (residues 26-44 of SEQ ID NO: 403)	
	182	97	50	28	3	3	0	1			
	97	147	175	178	181	181	182				

URE adaptors:

(SzKB1230-O12) 5'-cAcATcgTg TTgTT cacggATgTg ggA_{gg}AgA_{ct}ggTc-3' (SEQ ID NO: 400)
! | [RC] 5'-gaccaggatccatccatcc cAcATccgTg AAcAA cA_{gggg}ATgTg-3'
! | Recognition..... Stem..... loop..... Stem.....
! | FokI. FokI.

! Stem..... Loop. Stem..... Recognition.....

(SzKB1230-A17) 5'-cAcATcgTg TTgTT AcggATgTg ggAgAg' TggAgAcTgAgTc-3' (SEQ ID NO: 401)
 [RC] 5'-gactcgatccactcc cAcATccgTg AACAA cAcggATgTg'
 Recognition..... Stem..... loop. Stem.....
 FokI. FokI.

! Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-A27) 5'-cAcATcgTg TTgTT AcggATgTg ggTggAgAcTggTc-3' (SEQ ID NO: 402)
 [RC] 5'-gacgcgtccaggacc cAcATccgTg AACAA cAcggATgTg'
 Recognition..... Stem..... loop. Stem.....
 FokI. FokI.

! Stem..... Loop. Stem..... Recognition.....
 (SzKB1230-A11) 5'-cAcATcgTg TTgTT AcggATgTg ggTggAgAcTggTc-3' (SEQ ID NO: 403)
 [RC] 5'-gacgcgtccaggacc cAcATccgTg AACAA cAcggATgTg'
 Recognition..... Stem..... loop. Stem.....
 FokI. FokI.

What happens in the upper strand:

(SzKB1230-O12*)

5'-gac cca gtc | tcc a-tc ctc c-3' (residues 26-44 of SEQ ID NO: 400)
 | Site of cleavage in substrate

(SzKB1230-A17*)

5'-gac tca gtc | tcc a-ct ctc c-3' (residues 26-44 of SEQ ID NO: 401)

(SzKB1230-A27*)

5'-gac gca gtc | tcc a-gg cac c-3' (residues 26-44 of SEQ ID NO: 402)

(SzKB1230-A11*)

5'-gac gca gtc | tcc a-gc cac c-3' (residues 26-44 of SEQ ID NO: 403)

(kapextURE) 5' -ccTctactctTgTcAcAgTgCACAA gAC ATC cAg-3' ! sense strand (SEQ ID NO: 404)
 Scab. ApaLI.

(kapextUREPCR) 5' -ccTctactctTgTcAcAgTg-3' (SEQ ID NO: 405)
 Scab.

(kaBR01UR) 5' -ggAggATggA cTggATgTcT TgTgActgT gAcAAgAgTA gAgg-3' (SEQ ID NO: 406)
 ! [RC] 5' -cctctactctTgtcAcAgTgcACAA gAC ATC cAG tcc a-rc ctc c-3' ON above is R.C. of this one
 (kaBR02UR) 5' -ggAggTggA cTggATgTcT TgTgActgT gAcAAgAgTA gAgg-3' (SEQ ID NO: 407)
 ! [RC] 5' -cctctactctTgtcAcAgTgcACAA gAC ATC cAG tcc a-ct ctc c-3' ON above is R.C. of this one
 (kaBR03UR) 5' -ggAggTggA cTggATgTcT TgTgActgT gAcAAgAgTA gAgg-3' (SEQ ID NO: 408)
 ! [RC] 5' -cctctactctTgtcAcAgTgcACAA gAC ATC cAG tcc a-gg cac c-3' ON above is R.C. of this one
 (kaBR04UR) 5' -ggTggTggA cTggATgTcT TgTgActgT gAcAAgAgTA gAgg-3' (SEQ ID NO: 409)
 ! [RC] 5' -cctctactctTgtcAcAgTgcACAA gAC ATC cAG tcc a-gc cac c-3' ON above is R.C. of this one
 Scab.....ApalII.

Please delete Table 18 and replace it with the following table:

Table 18 Lambda URE adapters bases 13.3 to 19.3

! Number of sequences..... 128

! Id	Ntot	Number of mismatches.....								Sequence.....	Dot form.....	
		0	1	2	3	4	5	6	7			
! 1	58	45	7	1	0	0	0	2	2	VL133-2a2	gtctccggacatcgatc (residues 632-635 of SEQ ID NO: 410)	
! 2	16	10	1	0	1	0	1	0	2	VL133-3l	ggccgtggacacgtc .a.ag. (residues 632-635 of SEQ ID NO: 411)	
! 3	17	6	0	0	4	1	1	5	0	VL133-2c	gtctccgtacgtcagtcag. (residues 632-635 of SEQ ID NO: 412)	
! 4	37	3	0	10	4	4	3	7	4	2	VL133-1c	ggccccggggcaggggtc .g.c..a.g...agg. (residues 632-635 of SEQ ID NO: 413)
! 128	64	8	11	5	8	5	11	11	5			
! 64	72	83	88	96	101	112	123	128				

Stem.....loop. Stem..... Recognition.....
 (VL133-2a2) 5'-cAcATccgTg TTgTT cAcggATgTg gATcgActgTccAgggAgA-c-3' (SEQ ID NO: 410)
 ! [RC] 5'-gtctccgtacgtcgtac cAcATccgTg AAcaa cAcggATgTg-3'
 Recognition..... Stem..... Loop. Stem.....

Stem.....loop. Stem..... Recognition.....

(VL133-3l) 5'-cACATcgTg TTgTT cAcggATgTg gAcTgTcAgcAAggcc-3' (SEQ ID NO: 411)
! [RC] 5'-gccctggacacacgc cAcATccgTg AACAA cAcggATgTg-3'
! Recognition..... Stem..... Loop. Stem.....

! Stem..... loop. Stem..... Recognition.....
(VL133-2c) 5'-cACATcgTg TTgTT cAcggATgTg gAcTgAcTgTccAggAgAc-3' (SEQ ID NO: 412)
! [RC] 5'-gtcccgaggcgtacgc cAcATccgTg AACAA cAcggATgTg-3'
! Recognition..... Stem..... Loop. Stem.....

! Stem..... loop. Stem..... Recognition.....
(VL133-1c) 5'-cACATcgTg TTgTT cAcggATgTg gAccCTcTgccccTggggcc-3' (SEQ ID NO: 413)
! [RC] 5'-gcccccaggcaggaggc cAcATccgTg AACAA cAcggATgTg-3'

What happens in the top strand:

! site of cleavage in the upper strand
(VL133-2a2*) 5'-g tct cct g|ga cag tcg atc (residues 632-635 of SEQ ID NO: 410)
! (VL133-3l*) 5'-g gcc ttt g|ga cag aca gtc (residues 632-635 of SEQ ID NO: 411)
! (VL133-2c*) 5'-g tct cct g|ga cag tca gtc (residues 632-635 of SEQ ID NO: 412)

! (VL133-1c*) 5'-g gcc cca g|gg cag agg gtc (residues 632-635 of SEQ ID NO: 413)
! The following Extenders and Bridges all encode the AA sequence of 2a2 for codons 1-15
! 1
(ON_LamEx133) 5'-ccTcTgAcTgAgT gcA cAg -
! 2 3 4 5 6 7 8 9 10 11 12
AGt gcT TtA acC caA ccG gcT AGT gtT AGC ggT -
! 13 14 15
tcC ccG g ! 2a2 (SEQ ID NO: 414)
! 1

(ON_LamB1-133) [RC] 5'-ccTcTgActgAgT gcA cAg -

! 2 3 4 5 6 7 8 9 10 11 12
AGt gcT TtA acC caA ccG gct AGT gtT AGC ggT-

! 13 14 15

tcC ccG g ga cag tcg at-3'! **(SEQ ID NO: 415)** 2a2 *N.B.* the actual seq is the
reverse complement of the
one shown.

(ON_LamB2-133) [RC] 5'-ccTcTgActgAgT gcA cAg -

! 2 3 4 5 6 7 8 9 10 11 12
AGt gcT TtA acC caA ccG gct AGT gtT AGC ggT-

! 13 14 15

tcC ccG g ga cag acA gt-3'! **(SEQ ID NO: 416)** *N.B.* the actual seq is the
reverse complement of the
one shown.

(ON_LamB3-133) [RC] 5'-ccTcTgActgAgT gcA cAg -

! 2 3 4 5 6 7 8 9 10 11 12
AGt gcT TtA acC caA ccG gct AGT gtT AGC ggT-

! 13 14 15

tcC ccG g ga cag tcg tca gt-3'! **(SEQ ID NO: 417)** *N.B.* the actual seq is the
reverse complement of the
one shown.

(ON_LamB4-133) [RC] 5' -cCTctgActgAgT gca cAg -

! 2 3 4 5 6 7 8 9 10 11 12
AGt gcT TtA acc caA ccG gcT AGt gtT AGC ggT-s

! 13 14 15
tCC ccG g gg cag agg gt-3' ! 1c (SEQ ID NO: 418) N.B. the actual seq is the
reverse complement of the
one shown.

(ON_Lam133PCR) 5' -cCTctGACTgAGT gcA cAg AGt gc-3' (SEQ ID NO: 419)

Please delete Table 19 and replace it with the following table:

Table 19: Cleavage of 75 human light chains.

Enzyme	Recognition*	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AfIII	Cttaag	0	0	HC FR3
AgeI	Accggt	0	0	
AscI	GGcgcgcc	0	0	After LC
BglII	Agatct	0	0	
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcgc	0	0	
BstBI	TTcgaa	0	0	
DraIII	CACNNNgtg	0	0	
EagI	Cggccg	0	0	
FseI	GGCCGGcc	0	0	
FspI	TGCgca	0	0	
HpaI	GTTaac	0	0	
MfeI	Caattg	0	0	HC FR1
MluI	Acgcgt	0	0	
NcoI	Ccatgg	0	0	Heavy chain signal
NheI	Gctagc	0	0	HC/anchor linker
NotI	GCggccgc	0	0	In linker after HC
NruI	TCGcga	0	0	
PacI	TTAATTaa	0	0	
PmeI	GTAAaaac	0	0	
PmlI	CACgtg	0	0	
PvuI	CGATcg	0	0	
SacII	CCGCgg	0	0	
SalI	Gtcgac	0	0	
SfiI	GGCCNNNNnngcc	0	0	Heavy Chain signal (SEQ ID NO: 436)
SgfI	GCGATcgc	0	0	
SnaBI	TACgtta	0	0	
StuI	AGGcct	0	0	
XbaI	Tctaga	0	0	HC FR3
AatII	GACGTC	1	1	
AclI	AAcgtt	1	1	
AseI	ATtaat	1	1	
BsmI	GAATGCN	1	1	
BspEI	Tccgga	1	1	HC FR1 (SEQ ID NO: 437)
BstXI	CCANNNNNntgg	1	1	HC FR2 (SEQ ID NO: 438)
DrdI	GACNNNNnngtc	1	1	
HindIII	Aagctt	1	1	
PciI	Acatgt	1	1	
SapI	gaagagc	1	1	
ScaI	AGTact	1	1	
SexAI	Accwggt	1	1	
SpeI	Actagt	1	1	
TliI	Ctcgag	1	1	
XbaI	Ctcgag	1	1	
BcgI	cgannnnnntgc	2	2	<u>(SEQ ID NO: 439)</u>
BlpI	GCtnagc	2	2	
BssSI	Ctcgtg	2	2	
BstAPI	GCANNNNntgc	2	2	<u>(SEQ ID NO: 440)</u>
EspI	GCtnagc	2	2	
KasI	Ggcgcc	2	2	
PflMI	CCANNNNntgg	2	2	<u>(SEQ ID NO: 441)</u>

XmnI	GAANNnnnttc	2	2	<u>(SEQ ID NO: 442)</u>
ApaLI	Gtgcac	3	3	LC signal seq
NaeI	GCCggc	3	3	
NgoMI	Gccggc	3	3	
PvuII	CAGctg	3	3	
RsrII	CGgwccg	3	3	
BsrBI	GAGcgg	4	4	
BsrDI	GCAATGNNN	4	4	
BstZ17I	GTAtac	4	4	
EcoRI	Gaattc	4	4	
SphI	GCATGc	4	4	
SspI	AATatt	4	4	
AccI	GTmkac	5	5	
BcI	Tgatca	5	5	
BsmBI	Nnnnnngagacg	5	5	<u>(SEQ ID NO: 443)</u>
BsrGI	Tgtaca	5	5	
DraI	TTTaaa	6	6	
NdeI	CAtatg	6	6	HC FR4
SwaI	ATTTaaat	6	6	
BamHI	Ggatcc	7	7	
SacI	GAGCTc	7	7	
BciVI	GTATCCNNNNNN	8	8	<u>(SEQ ID NO: 444)</u>
BsaBI	GATNNnnatc	8	8	<u>(SEQ ID NO: 619)</u>
NsiI	ATGCAt	8	8	
Bsp120I	Gggccc	9	9	CH1
ApaI	GGGCCc	9	9	CH1
PspOOMI	Gggccc	9	9	
BspHI	Tcatga	9	11	
EcoRV	GATatc	9	9	
AhdI	GACNNNNnngtc	11	11	<u>(SEQ ID NO: 445)</u>
BbsI	GAAGAC	11	14	
PsII	TTAtaa	12	12	
BsaI	GGTCTCNnnnn	13	15	<u>(SEQ ID NO: 446)</u>
XmaI	Cccggg	13	14	
AvaI	Cycgrg	14	16	
BglI	GCCNNNNnggc	14	17	<u>(SEQ ID NO: 447)</u>
AlwNI	CAGNNNctg	16	16	
BspMI	ACCTGC	17	19	
XcmI	CCANNNNNnnnntgg	17	26	<u>(SEQ ID NO: 448)</u>
BstEII	Ggtnacc	19	22	HC FR4
Sse8387I	CCTGCAGg	20	20	
AvrII	Cctagg	22	22	
HincII	GTYrac	22	22	
BsgI	GTGCAG	27	29	
MscI	TGGcca	30	34	
BseRI	NNnnnnnnnnnctcctc	32	35	<u>(SEQ ID NO: 449)</u>
Bsu36I	CCtnagg	35	37	
PstI	CTGCAg	35	40	
EciI	nnnnnnnnnnntccgcc	38	40	<u>(SEQ ID NO: 450)</u>
PpuMI	RGgwccy	41	50	
StyI	Ccwwgg	44	73	
EcoO109I	RGgnccy	46	70	
Acc65I	Ggtacc	50	51	
KpnI	GGTACc	50	51	
BpmI	ctccag	53	82	
Avall	Ggwcc	71	124	

* cleavage occurs in the top strand after the last upper-case base.
 For REs that cut palindromic sequences, the lower strand is cut at the symmetrical site.

Please delete Table 20 and replace it with the following table:

Table 20: Cleavage of 79 human heavy chains

Enzyme	Recognition	Nch	Ns	Planned location of site
AfeI	AGCgct	0	0	
AflIII	Cttaag	0	0	HC FR3
AscI	GGcgcgcc	0	0	After LC
BsiWI	Cgtacg	0	0	
BspDI	ATcgat	0	0	
BssHII	Gcgcbc	0	0	
FseI	GGCCGGcc	0	0	
HpaI	GTtaac	0	0	
NheI	Gcttagc	0	0	HC Linker
NotI	GCggccgc	0	0	In linker, HC/anchor
NruI	TCGcga	0	0	
NsII	ATGCAt	0	0	
PacI	TTAATTaa	0	0	
PciI	Acatgt	0	0	
PmeI	GTTTaaac	0	0	
PvuI	CGATcg	0	0	
RsrII	CGgwccg	0	0	
SapI	gaagagc	0	0	
SfiI	GGCCNNNNnnggcc	0	0	HC signal seq <u>(SEQ ID NO: 420)</u>
SgfI	GCGATcgc	0	0	
SwaI	ATTtaaat	0	0	
AclI	AAcgtt	1	1	
AgeI	Accggt	1	1	
AseI	ATtaat	1	1	
AvrII	Cctagg	1	1	
BsmI	GAATGCN	1	1	
BsrBI	GAGcgg	1	1	
BsrDI	GCAATGNNn	1	1	
DraI	TTTaaa	1	1	
FspI	TGCgca	1	1	
HindIII	Aagctt	1	1	
MfeI	Caattg	1	1	HC FR1
NaeI	GCCggc	1	1	
NgoMI	Gccggc	1	1	
SpeI	Actagt	1	1	
Acc65I	Ggtacc	2	2	
BstBI	TTcgaat	2	2	
KpnI	GGTACc	2	2	
MluI	Acgcgt	2	2	
NcoI	Ccatgg	2	2	In HC signal seq
NdeI	CAtatg	2	2	HC FR4
PmlI	CACgtg	2	2	
XcmI	CCANNNNNnnnnntgg	2	2	<u>(SEQ ID NO: 421)</u>
BcgI	cgannnnnnntgc	3	3	<u>(SEQ ID NO: 422)</u>
BclI	Tgatca	3	3	

BglI	GCCNNNNnggc	3	3	<u>(SEQ ID NO: 423)</u>
Bsabi	GATNNnnatc	3	3	<u>(SEQ ID NO: 424)</u>
BsrGI	Tgtaca	3	3	
Snabi	TACgtta	3	3	
Sse8387I	CCTGCAGg	3	3	
ApalI	Gtgcac	4	4	LC Signal/FR1
BspHI	Tcatga	4	4	
BssSI	Ctcgtg	4	4	
PsII	TTAtaa	4	5	
SphI	GCATGc	4	4	
AhdI	GACNNNNngtc	5	5	<u>(SEQ ID NO: 425)</u>
BspEI	Tccgga	5	5	HC FR1
MscI	TGGGcca	5	5	
SacI	GAGCTc	5	5	
ScalI	AGTact	5	5	
SexAI	Accwggt	5	6	
SspI	AATatt	5	5	
TliI	Ctcgag	5	5	
XhoI	Ctcgag	5	5	
BbsI	GAAGAC	7	8	
BstAPI	GCANNNNntgc	7	8	<u>(SEQ ID NO: 426)</u>
BstZ17I	GTAtac	7	7	
EcoRV	GATatc	7	7	
EcoRI	Gaattc	8	8	
BlpI	GCtnagc	9	9	
Bsu36I	CCtnagg	9	9	
DraIII	CACNNNgtg	9	9	
EspI	GCtnagc	9	9	
StuI	AGGcct	9	13	
XbaI	Tctaga	9	9	HC FR3
Bsp120I	Gggccc	10	11	CH1
Apal	GGGCCc	10	11	CH1
PspOOMI	Gggccc	10	11	
BciVI	GTATCCNNNNNN	11	11	<u>(SEQ ID NO: 427)</u>
SalI	Gtcgac	11	12	
DrdI	GACNNNNngtc	12	12	<u>(SEQ ID NO: 428)</u>
KasI	Ggcgcc	12	12	
XmaI	Cccggg	12	14	
BglII	Agatct	14	14	
HincII	GTYrac	16	18	
BamHI	Ggatcc	17	17	
PflMI	CCANNNNntgg	17	18	<u>(SEQ ID NO: 429)</u>
BsmBI	Nnnnnngagacg	18	21	<u>(SEQ ID NO: 430)</u>
BstXI	CCANNNNNntgg	18	19	HC FR2 (SEQ ID NO: 431)
XmnI	GAANNnnttc	18	18	<u>(SEQ ID NO: 432)</u>
SacII	CCGCgg	19	19	
PstI	CTGCAg	20	24	
PvullI	CAGctg	20	22	
AvaI	Cycgrg	21	24	
EagI	Cggccg	21	22	
AatII	GACGTc	22	22	
BspMI	ACCTGC	27	33	
AccI	GTmkac	30	43	
StyI	Ccwwgg	36	49	
AlwNI	CAGNNNctg	38	44	
BsaI	GGTCTCNnnnn	38	44	<u>(SEQ ID NO: 433)</u>
PpuMI	RGgwccy	43	46	

BsgI	GTGCAG	44	54	
BseRI	NNnnnnnnnnnctcctc	48	60	<u>(SEQ ID NO: 434)</u>
EciI	nnnnnnnnnnntccgcc	52	57	<u>(SEQ ID NO: 435)</u>
BstEII	Ggttnacc	54	61	HC Fr4, 47/79 have one
EcoO109I	RGgnccy	54	86	
BpmI	ctccag	60	121	
AvaiI	Ggwcc	71	140	

Please delete Table 21 and replace it with the following table:

Table 21: MALIA3, annotated

! MALIA3 9532 bases

1

(SEO ID NO: 451)

1 aat gct act act att agt aga att gat gcc acc ttt tca gct cgc gcc
gene ii continued

```

49 cca aat gaa aat ata gct aaa cag gtt att gac cat ttg cga aat gta
97 tct aat ggt caa act aaa tct act cgt tcg cag aat tgg gaa tca act
145 gtt aca tgg aat gaa act tcc aga cac cgt act tta gtt gca tat tta
193 aaa cat gtt gag cta cag cac cag att cag caa tta agc tct aag cca
241 tcc gca aaa atg acc tct tat caa aag gag caa tta aag gta ctc tct
289 aat cct gac ctg ttg gag ttt gct tcc ggt ctg gtt cgc ttt gaa gct
337 cga att aaa acg cga tat ttg aag tct ttc ggg ctt cct ctt aat ctt
385 ttt gat gca atc cgc ttt gct tct gac tat aat agt cag ggt aaa gac
433 ctg att ttt gat tta tgg tca ttc tcg ttt tct gaa ctg ttt aaa gca
481 ttt gag ggg gat tca ATG aat att tat gac gat tcc gca gta ttg gac
! RBS?..... Start gene x, ii continues
529 gct atc cag tct aaa cat ttt act att acc ccc tct ggc aaa act tct
577 ttt gca aaa gcc tct cgc tat ttt ggt ttt tat cgt cgt ctg gta aac
625 gag ggt tat gat agt gtt gct ctt act atg cct cgt aat tcc ttt tgg
673 cgt tat gta tct gca tta gtt gaa tgt ggt att cct aaa tct caa ctg
721 atg aat ctt tct acc tgt aat aat gtt gtt ccg tta gtt cgt ttt att
769 aac gta gat ttt tct tcc caa cgt cct gac tgg tat aat gag cca gtt

```

817 ctt aaa atc gca TAA

(SEQ. ID. NO.: 623)

(SEQ ID NO: 623) 55 Q10 T15

843 ATG att aaa gtt gaa att aaa cca tct caa gcc caa ttt act act cgt
Start gene V

S17 S20 P25 E30

891 tct ggt gtt tct cgt cag ggc aag cct tat tca ctg aat gag cag ctt

V3.5 E1.0 V4.5

939 tgt tac gtt gat ttg ggt aat gaa tat ccc att ctt ctc aag att act

DEO DEE DEG DEG

987 ctt gat gaa ggt cag cca gcc tat gcg cct ggt cTG TAC Acc gtt cat
BsrGI

! L65 V70 S75 R80
 1035 ctg tcc tct ttc aaa gtt ggt caq ttc ggt tcc ctt atg att gac cgt

! P85 K87 end of V
1083 ctg cqc ctc qtt ccq qct aaq TAA C

```

!
! 1108 ATG gag cag gtc gcg gat ttc gac aca att tat cag gcg atg
! Start gene VII
!
! 1150 ata caa atc tcc gtt gta ctt tgt ttc gcg ctt ggt ata atc
!
! VII and IX overlap.
! .... S2 V3 L4 V5 (SEQ ID NO: 624) S10
! 1192 gct ggg ggt caa agA TGA gt gtt tta gtg tat tct ttc gcc tot ttc
gtt
!
! End VII
! | start IX
! L13 W15 G20 T25
E29
! 1242 tta ggt tgg tgc ctt cgt agt ggc att acg tat ttt acc cgt tta atg
gaa
!
! 1293 act tcc tc
!
! .... stop of IX, IX and VIII overlap by four bases
! 1301 ATG aaa aag tct tta gtc ctc aaa gcc tct gta gcc gtt gct acc ctc
! Start signal sequence of viii.
!
! 1349 gtt ccg atg ctg tct ttc gct gct gag ggt gac gat ccc gca aaa gcg
! mature VIII --->
1397 gcc ttt aac tcc ctg caa gcc tca gcg acc gaa tat atc ggt tat gcg
1445 tgg gcg atg gtt gtt gtc att
1466 gtc ggc gca act atc ggt atc aag ctg ttt aag
1499 aaa ttc acc tcg aaa gca ! 1515
!
! ..... -35 ...
!
! 1517 agc tga taaaaccgat acaattaaag gtccttttg
! .... -10 ...
!
! 1552 gagcctttt ttttGGAGAt ttt ! S.D. underlined
!
! <----- III signal sequence ----->
! M K K L L F A I P L V (SEQ ID NO: 452)
! 1575 caac GTG aaa aaa tta tta ttc gca att cct tta gtt ! 1611
!
! V P F Y S H S A Q
! 1612 gtt cct ttc tat tct cac aGT gca Cag tCT
! ApaLI...
!
! 1642 GTC GTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG
AGG GTC ACC ATC TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA
!
! BstEII...
1729 GGT TAT GAT GTA CAC TGG TAC CAG CAG CTT CCA GGA ACA GCC CCC
AAA
1777 CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC CCT GAC
CGA
1825 TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT
1870 GGG CTC CAG GCT GAG GAT GAG GCT GAT TAT
1900 TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT
1930 GGC CTT TAT GTC TTC GGA ACT GGG ACC AAG GTC ACC GTC
!
! BstEII...
1969 CTA GGT CAG CCC AAG GCC AAC CCC ACT GTC ACT

```

2002 CTG TTC CCG CCC TCC TCT GAG GAG CTC CAA GCC AAC AAG GCC ACA
 CTA
 2050 GTG TGT CTG ATC AGT GAC TTC TAC CCG GGA GCT GTG ACA GTG GCC
 TGG
 2098 AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA
 CCC
 2146 TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAT CTG AGC
 CTG
 2194 ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC
 ACG
 2242 CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT
 TCA
 2290 TAA TAA ACCG CCTCCACCGG GCGCGCCAAT TCTATTCAA GGAGACAGTC ATA
 ! Ascl.....
 ! (SEQ ID NO: 453)
 ! PelB signal----->
 ! M K Y L L P T A A A G L L L L
 2343 ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC
 !
 ! 16 17 18 19 20 21 22
 ! A A Q P A M A
 2388 gcG GCC cag ccG GCC atg gcc
 ! SfiI.....
 ! NgoMI...(1/2)
 ! NcoI.....
 !
 ! FR1 (DP47/V3-23)-----
 ! 23 24 25 26 27 28 29 30
 ! E V Q L L E S G
 2409 gaa|gtt|CAA|TTG|tta|gag|tct|ggt|
 ! MfeI |
 !
 ! -----FR1-----
 ! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
 ! G G L V Q P G G S L R L S C A
 2433 |ggc|ggt|ctt|gtt|cag|cct|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
 !
 ! -----FR1----->|...CDR1.....|---FR2---
 ! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
 ! A S G F T F S S Y A M S W V R
 2478 |gct|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|gtt|cgC|
 ! BspEI | BsiWI |
 ! BstXI.
 !
 ! -----FR2----->|...CDR2.....
 ! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
 ! Q A P G K G L E W V S A I S G
 2523 |CAa|gct|ccT|GGt|aaa|ggt|ttg|gag|tgg|gtt|tct|gct|atc|tct|ggt|
 ! ...BstXI |
 !
 !CDR2.....|...|---FR3---
 ! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
 ! S G G S T Y Y A D S V K G R F
 2568 |tct|ggt|ggc|agt|act|tac|tat|gct|gac|tcc|gtt|aaa|ggt|cgC|ttc|
 !
 ! -----FR3-----
 ! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105

```

!
!      T   I   S   R   D   N   S   K   N   T   L   Y   L   Q   M
! 2613 |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|
!           | XbaI |
!
!      ---FR3----->
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      N   S   L   R   A   E   D   T   A   V   Y   Y   C   A   K
! 2658 |aac|agC|TTA|AGg|gct|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa|
!           |AflIII |           | PstI |
!
!      .....CDR3.....|---FR4-----
!      121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
!      D   Y   E   G   T   G   Y   A   F   D   I   W   G   Q   G
! 2703 |gac|tat|gaa|ggt|act|ggt|tat|gct|ttc|gaC|ATA|TGg|ggt|caa|ggt|
!           | NdeI | (1/4)
!
!      -----FR4----->
!      136 137 138 139 140 141 142
!      T   M   V   T   V   S   S
! 2748 |act|atG|GTC|ACC|gtc|tct|agt
!           | BstEII |
!
! From BstEII onwards, pV323 is same as pCES1, except as noted.
! BstEII sites may occur in light chains; not likely to be unique in
final
vector.
!
!
!      143 144 145 146 147 148 149 150 151 152
!      A   S   T   K   G   P   S   V   F   P
! 2769   gcc tcc acc aaG GGC CCA tcg GTC TTC ccc
!           | Bsp120I.           | BbsI... (2/2)
!           | ApaI.... |
!
!
!      153 154 155 156 157 158 159 160 161 162 163 164 165 166 167
!      L   A   P   S   S   K   S   T   S   G   G   T   A   A   L
! 2799 ctg gca ccC TCC TCc aag agc acc tct ggg ggc aca gcg gcc ctg
!           | BseRI... (2/2)
!
!
!      168 169 170 171 172 173 174 175 176 177 178 179 180 181 182
!      G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S
! 2844   ggc tgc ctg GTC AAG GAC TAC TTC CCc gaA CCG GTg acg gtg tcg
!           | AgeI.... |
!
!
!      183 184 185 186 187 188 189 190 191 192 193 194 195 196 197
!      W   N   S   G   A   L   T   S   G   V   H   T   F   P   A
! 2889 tgg aac tca GGC GCC ctg acc agc ggc gtc cac acc ttc ccg gct
!           | KasI... (1/4)
!
!
!      198 199 200 201 202 203 204 205 206 207 208 209 210 211 212
!      V   L   Q   S   S   G   L   Y   S   L   S   S   V   V   T
! 2934   gtc cta cag tCt agc GGa ctc tac tcc ctc agc agc gta gtg acc
!           | (Bsu36I...) (knocked out)
!
!
!      213 214 215 216 217 218 219 220 221 222 223 224 225 226 227
!      V   P   S   S   S   L   G   T   Q   T   Y   I   C   N   V
! 2979   gtg ccC tCt tct agc tTG Ggc acc cag acc tac atc tgc aac gtg
!           | (BstXI.....) N.B. destruction of BstXI & BpmI
sites.
!
```

```

!
! 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242
!   N   H   K   P   S   N   T   K   V   D   K   K   V   E   P
3024  aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc
!
! 243 244 245
!   K   S   C   A   A   A   H   H   H   H   H   H   H   S   A
3069  aaa tct tgt GCG GCC GCT cat cac cac cat cat cac tct gct
!   NotI.....
!
!   E   Q   K   L   I   S   E   E   D   L   N   G   A   A
3111  gaa caa aaa ctc atc tca gaa gag gat ctg aat ggt gcc gca
!
!   D   I   N   D   D   R   M   A   S   G   A
3153  GAT ATC aac gat gat cgt atg   gct AGC   ggc gcc
!   rEK cleavage site..... NheI... KasI...
!   EcoRV..
!
! Domain 1 -----
!
!   A   E   T   V'   E   S   C   L   A
3183  gct gaa act gtt gaa agt tgt tta gca
!
!
!   K   P   H   T   E   IN   S   F
3210  aaa ccc cat aca gaa aat tca ttt
!
!   T   N   V   W   K   D   D   K   T
3234  aCT AAC GTC TGG AAA GAC GAC AAA Act
!
!   L   D   R   Y   A   N   Y   E   G   C   L   W   N   A   T   G
V
3261  tta gat cgt tac gct aac tat gag ggt tgt ctg tgG AAT GCT aca ggc
gtt
!
!   BsmI _____
!
!   V   V   C   T   G   D   E   T   Q   C   Y   G   T   W   V   P
I
3312  gta gtt tgt act ggt GAC GAA ACT CAG TGT TAC GGT ACA TGG GTT cct
att
!
!   G   L   A   I   P   E   N
3363  ggg ctt gct atc cct gaa aat
!
! L1 linker -----
!
!   E   G   G   G   S   E   G   G   G   S
3384  gag ggt ggt ggc tct gag ggt ggc ggt tct
!
!   E   G   G   G   S   E   G   G   G   T
3414  gag ggt ggc ggt tct gag ggt ggc ggt act
!
! Domain 2 -----
3444  aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat atc
aac
3495  cct ctc gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat
cct
3546  aat cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
aat
!
!   BseRI _____

```

3597 aat agg ttc cga aat agg cag ggg gca tta act gtt tat acg ggc act
 3645 gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act cct
 3693 gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttC AGA
 ! AlwNI
 3741 GAC TGc gct ttc cat tct ggc ttt aat gaa gat cca ttc gtt tgt gaa
 ! AlwNI
 3789 tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct
 !
 3834 ggc ggc ggc tct
 ! start L2

3846 ggt ggt ggt tct
 3858 ggt ggc ggc tct
 3870 gag ggt ggc tct gag ggt ggc ggt tct
 3900 gag ggt ggc ggc tct gag gga ggc ggt tcc
 3930 ggt ggt ggc tct ggt ! end L2

!

! Domain 3

(SEQ ID NO: 454)

! S G D F D Y E K M A N A N K G A
 3945 tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct
 !

! M T E N A D E N A L Q S D A K G
 3993 atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc

!

! K L D S V A T D Y G A A I D G F
 4041 aaa ctt gat tct gtc gct act gat tac ggt gct gct atc gat ggt ttc

!

! I G D V S G L A N G N G A T G D
 4089 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat

!

! F A G S N S Q M A Q V G D G D N
 4137 ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat

!

! S P L M N N F R Q Y L P S L P Q
 4185 tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa

!

! S V E C R P F V F S A G K P Y E
 4233 tcg gtt gaa tgt cgc cct ttt gtc ttt agc gct ggt aaa cca tat gaa

!

! F S I D C D K I N L F R
 4281 ttt tct att gat tgt gac aaa ata aac tta ttc cgt

!

End Domain 3

!

! G V F A F L L Y V A T F M Y V F140
 4317 ggt gtc ttt gcg ttt ctt tta tat gtt gct gcc acc ttt atg tat gta ttt

!

start transmembrane segment

!

! S T F A N I L
 4365 tct acg ttt gct aac ata ctg

!

! R N K E S
 4386 cgt aat aag gag tct TAA ! stop of iii
 Intracellular anchor.

!

(SEQ ID NO: 455)

M1 P2 V L L5 G I P L L10 L R F L G15

4404 tc ATG cca gtt ctt ttg ggt att ccg tta tta ttg cgt ttc ctc ggt
Start VI

4451 ttc ctt ctg gta act ttg ttc ggc tat ctg ctt act ttt ctt aaa aag
4499 ggc ttc ggt aag ata gct att gct att tca ttg ttt ctt gct ctt att
4547 att ggg ctt aac tca att ctt gtg ggt tat ctc tct gat att agc gct
4595 caa tta ccc tct gac ttt gtt cag ggt gtt cag tta att ctc ccg tct
4643 aat gcg ctt ccc tgt ttt tat gtt att ctc tct gta aag gct gct att
4691 ttc att ttt gac gtt aaa caa aaa atc gtt tct tat ttg gat tgg gat

(SEQ ID NO: 456)

M1	A2	V3	F5													L10	G13		
4739	aaa	TAA	t	ATG	gct	gtt	tat	ttt	gta	act	ggc	aaa	tta	ggc	tct	gga			
end VI				Start gene I															
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28					
K	T	L	V	S	V	G	K	I	Q	D	K	I	V	A					
4785	aag	acg	ctc	gtt	agc	gtt	ggt	aag	att	cag	gat	aaa	att	gta	gct				
29	30	31	32	33	34	35	36	37	38	39	40	41	42	43					
G	C	K	I	A	T	N	L	D	L	R	L	Q	N	L					
4830	ggg	tgc	aaa	ata	gca	act	aat	ctt	gat	tta	agg	ctt	caa	aac	ctc				
44	45	46	47	48	49	50	51	52	53	54	55	56	57	58					
P	Q	V	G	R	F	A	K	T	P	R	V	L	R	I					
4875	ccg	caa	gtc	ggg	agg	ttc	gct	aaa	acg	cct	cgc	gtt	ctt	aga	ata				
59	60	61	62	63	64	65	66	67	68	69	70	71	72	73					
P	D	K	P	S	I	S	D	L	L	A	I	G	R	G					
4920	ccg	gat	aag	cct	tct	ata	tct	gat	ttg	ctt	gct	att	ggg	cgc	ggt				
74	75	76	77	78	79	80	81	82	83	84	85	86	87	88					
N	D	S	Y	D	E	N	K	N	G	L	L	V	L	D					
4965	aat	gat	tcc	tac	gat	gaa	aat	aaa	aac	ggc	ttg	ctt	gtt	ctc	gat				
89	90	91	92	93	94	95	96	97	98	99	100	101	102	103					
E	C	G	T	W	F	N	T	R	S	W	N	D	K	E					
5010	gag	tgc	ggt	act	tgg	ttt	aat	acc	cgt	tct	tgg	aat	gat	aag	gaa				
104	105	106	107	108	109	110	111	112	113	114	115	116	117	118					
R	Q	P	I	I	D	W	F	L	H	A	R	K	L	G					
5055	aga	cag	ccg	att	att	gat	tgg	ttt	cta	cat	gct	cgt	aaa	tta	gga				
119	120	121	122	123	124	125	126	127	128	129	130	131	132	133					
W	D	I	I	F	L	V	Q	D	L	S	I	V	D	K					
5100	tgg	gat	att	att	ttt	ctt	gtt	cag	gac	tta	tct	att	gtt	gat	aaa				
134	135	136	137	138	139	140	141	142	143	144	145	146	147	148					
Q	A	R	S	A	L	A	E	H	V	V	Y	C	R	R					
5145	cag	gcg	cgt	tct	gca	tta	gct	gaa	cat	gtt	gtt	tat	tgt	cgt	cgt				
149	150	151	152	153	154	155	156	157	158	159	160	161	162	163					
L	D	R	I	T	L	P	F	V	G	T	L	Y	S	L					
5190	ctg	gac	aga	att	act	tta	cct	ttt	gtc	ggt	act	tta	tat	tct	ttt				
164	165	166	167	168	169	170	171	172	173	174	175	176	177	178					
I	T	G	S	K	M	P	L	P	K	L	H	V	G	V					
5235	att	act	ggc	tcg	aaa	atg	cct	ctg	cct	aaa	tta	cat	qtt	qgc	qtt				

```

!
!      179 180 181 182 183 184 185 186 187 188 189 190 191 192 193
!      V   K   Y   G   D   S   Q   L   S   P   T   V   E   R   W
5280 gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg
!
!      194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
!      L   Y   T   G   K   N   L   Y   N   A   Y   D   T   K   Q
5325 ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag
!
!      209 210 211 212 213 214 215 216 217 218 219 220 221 222 223
!      A   F   S   S   N   Y   D   S   G   V   Y   S   Y   L   T
5370 gct ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg
!
!      224 225 226 227 228 229 230 231 232 233 234 235 236 237 238
!      P   Y   L   S   H   G   R   Y   F   K   P   L   N   L   G
5415 cct tat tta tca cac ggt cggt tat ttc aaa cca tta aat tta ggt
!
!      239 240 241 242 243 244 245 246 247 248 249 250 251 252 253
!      Q   K   M   K   L   T   K   I   Y   L   K   K   F   S   R
5460 cag aag atg aaa tta act aaa ata tat ttg aaa aag ttt tct cgc
!
!      254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
!      V   L   C   L   A   I   G   F   A   S   A   F   T   Y   S
5505 gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt aca tat agt
!
!      269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
!      Y   I   T   Q   P   K   P   E   V   K   K   V   V   S   Q
5550 tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc tct cag
!
!      284 285 286 287 288 289 290 291 292 293 294 295 296 297 298
!      T   Y   D   F   D   K   F   T   I   D   S   S   Q   R   L
5595 acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt ctt
!
!      299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
!      N   L   S   Y   R   Y   V   F   K   D   S   K   G   K   L
5640 aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa TTA
!      PacI
!
!      314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
!      I   N   S   D   D   L   Q   K   Q   G   Y   S   L   T   Y
5685 ATT AAt agc gac gat tta cag aag caa ggt tat tca ctc aca tat
!      PacI
!
!      329 330 331 332 333 334 335 336 337 338 339 340 341 342 343
!      i   I   D   L   C   T   V   S   I   K   K   G   N   S   N   E
!      (SEQ ID NO: 620)
!      iv
5730 att gat tta tgt act gtt tcc att aaa aaa ggt aat tca aAT Gaa
!      Start IV
!
!      344 345 346 347 348 349
!      i   I   V   K   C   N   .End of I
!      iv   L3   L   N5   V   I7   N   F   V10
5775 att gtt aaa tgt aat TAA T TTT GTT
!      IV continued.....
5800 ttc ttg atg ttt gtt tca tca tct tct ttt gct cag gta att gaa atg
5848 aat aat tcg cct ctg cgc gat ttt gta act tgg tat tca aag caa tca
5896 ggc gaa tcc gtt att gtt tct ccc gat gta aaa ggt act gtt act gta

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5944 tat tca tct gac gtt aaa cct gaa aat cta cgc aat ttc ttt att tct
 5992 gtt tta cgt gct aat aat ttt gat atg gtt ggt tca att cct tcc ata
 6040 att cag aag tat aat cca aac aat cag gat tat att gat gaa ttg cca
 6088 tca tct gat aat cag gaa tat gat gat aat tcc gct cct tct ggt ggt
 6136 ttc ttt gtt ccg caa aat gat aat gtt act caa act ttt aaa att aat
 6184 aac gtt ccg gca aag gat tta ata cga gtt gtc gaa ttg ttt gta aag
 6232 tct aat act tct aaa tcc tca aat gta tta tct att gac ggc tct aat
 6280 cta tta gtt gtt TCT gca cct aaa gat att tta gat aac ctt cct caa
 ! ApaLI removed
 6328 ttc ctt tct act gtt gat ttg cca act gac cag ata ttg att gag ggt
 6376 ttg ata ttt gag gtt cag caa ggt gat gct tta gat ttt tca ttt gct
 6424 gct ggc tct cag cgt ggc act gtt gca ggc ggt gtt aat act gac cgc
 6472 ctc acc tct gtt tta tct tct gct ggt ggt tcg ttc ggt att ttt aat
 6520 ggc gat gtt tta ggg cta tca gtt cgc gca tta aag act aat agc cat
 6568 tca aaa ata ttg tct gtg cca cgt att ctt acg ctt tca ggt cag aag
 6616 ggt tct atc tct gtT GGC CAG aat gtc cct ttt att act ggt cgt gtg
 ! MscI
 6664 act ggt gaa tct gcc aat gta aat aat cca ttt cag acg att gag cgt
 6712 caa aat gta ggt att tcc atg agc gtt ttt cct gtt gca atg gct ggc
 6760 ggt aat att gtt ctg gat att acc agc aag gcc gat agt ttg agt tct
 6808 tct act cag gca agt gat gtt att act aat caa aga agt att gct aca
 6856 acg gtt aat ttg cgt gat gga cag act ctt tta ctc ggt ggc ctc act
 6904 gat tat aaa aac act tct caa gat tct ggc gta ccg ttc ctg tct aaa
 6952 atc cct tta atc ggc ctc ctg ttt agc tcc cgc tct gat tcc aac gag
 7000 gaa agc acg tta tac gtg ctc gtc aaa gca acc ata gta cgc gcc ctg
 7048 TAG cggcgcatt
 ! End IV
 7060 aagcgcggcg ggtgtgggtgg ttacgcgcag cgtgaccgct acacttgcca
 ggcgccttagc
 7120 gcccgccttct ttgcgtttct tcccttcctt tctcgccacg ttcGCCGGCT
 ttccccgtca
 ! NgoMI
 7180 agctctaaat cgggggctcc ctttagggtt ccgatttagt gctttacggc
 acctcgaccc
 7240 caaaaaactt gatttgggtg atggttCACG TAGTGggcca tcgcccctgat
 agacggttt
 ! DraIII
 7300 tcgccccttG ACGTTGGAGT Ccacgttctt taatagtggaa ctcttgttcc
 aaactggaac
 ! DrdI
 7360 aacactcaac cctatctcg gctattcttt tgatttataa gggattttgc
 cgatttcgga
 7420 accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg
 cttgctgcaa
 7480 ctctctcagg gccaggcggt gaagggcaat CAGCTGttgc cCGTCTCact
 ggtaaaaaga
 ! PvuII. BsmBI.
 7540 aaaaccaccc tGGATCC AAGCTT
 ! BamHI HindIII (%)

!
 Insert carrying bla gene

7563 gcaggtg gcactttcg gggaaatgtg cgcgaaaccc
 7600 ctattgttt attttctaa atacattcaa atatGTATCC gctcatgaga
 caataaccct

!
 BciVI

7660 gataaatgct tcaataatat tgaaaaAGGA AGAgt
 !
 RBS.???

!
 Start bla gene

7695 ATG agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg gca
 ttt

7746 tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta aaa gat
 gct

7797 gaa gat cag ttg ggC gCA CGA Gtg ggt tac atc gaa ctg gat ctc aac
 agc

!
 BssSI...

!
 ApaLI removed

7848 ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg
 agc

7899 act ttt aaa gtt ctg cta tgt cat aca cta tta tcc cgt att gac gcc
 ggg

7950 caa gaG CAA CTC GGT CGC cgg gcg cgg tat tct cag aat gac ttg gtt
 gAG

!
 BcgI_____

ScaI

8001 TAC Tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga
 gaa

!
 ScaI_
 8052 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
 ctt

8103 ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg cac aac
 atg

!
 PvuI

8154 ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa
 gcc

8205 ata cca aac gac gag cgt gac acc acg atg cct gta gca atg cca aca
 acg

8256 tTG CGC Aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa
 caa

!
 FspI....

!
 8307 tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc
 tcg

8358 GCC ctt ccG GCt ggc tgg ttt att gct gat aaa tct gga gcc ggt gag
 cgt

!
 BglI

8409 gGG TCT Cgc ggt atc att gca gca ctg ggg cca gat ggt aag ccc tcc
 cgt

!
 BsaI

8460 atc gta gtt atc tac acG ACg ggg aGT Cag gca act atg gat gaa cga
 aat

!
 AhDI

8511 aga cag atc gct gag ata ggt gcc tca ctg att aag cat tgg TAA ctgt
 !
 stop

8560 cagaccaagt ttactcatat atactttaga ttgattaaa acttcatttt
 taatttaaaa

8620 ggatcttaggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa
 cgtgagttt

8680 cgttccactg tacgtaagac cccc

```

8704 AAGCTT  GTCGAC tgaa tggcgaatgg cgctttgcct
! HindIII  SalI..
! (2/2)  HincII
8740 ggttccggc accagaagcg gtgccggaaa gctggctgga gtgcgatctt
!
8790 CCTGAGG
! Bsu36I_
8797 ccgat actgtcgctcg tcccctcaaa ctggcagatg
8832 cacggttacg atgcgcccatttacaccaac gtaacctatc ccattacgg
caatccggcg
8892 tttgttccca cggagaatcc gacgggttgt tactcgctca catttaatgt
tgatgaaagc
8952 tggctacagg aaggccagac gcgaattattt tttgatggcg ttcctattgg
ttaaaaaatg
9012 agctgattta acaaaaattt aacgcgaattt ttaacaaaat attaacgttt
acaATTAAA
!
SwaI...
9072 Tatttgctta tacaatcttc ctgttttgg ggctttctg attatcaacc GGGGTAcat
! RBS?
9131 ATG att gac atg cta gtt tta cga tta ccg ttc atc gat tct ctt gtt
tgc
! Start gene II
9182 tcc aga ctc tca ggc aat gac ctg ata gcc ttt gtA GAT CTc tca aaa
ata
!
9233 gct acc ctc tcc ggc atg aat tta tca gct aga acg gtt gaa tat cat
att
9284 gat ggt gat ttg act gtc tcc ggc ctt tct cac cct ttt gaa tct tta
cct
9335 aca cat tac tca ggc att gca ttt aaa ata tat gag ggt tct aaa aat
ttt
9386 tat cct tgc gtt gaa ata aag gct tct ccc gca aaa gta tta cag ggt
cat
9437 aat gtt ttt ggt aca acc gat tta gct tta tgc tct gag gct tta ttg
ctt
9488 aat ttt gct aat tct ttg cct tgc ctg tat gat tta ttg gat gtt !
9532
! gene II continues

```

Please delete Table 21B and replace it with the following table:

Table 21B: Sequence of MALIA3, condensed

LOCUS MALIA3 9532 CIRCULAR

ORIGIN

(SEQ ID NO: 451)

1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTCA	CTCGCGCCCC	AAATGAAAAT
61	ATAGCTAAAC	AGGTTATTGA	CCATTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT
121	CGTCGCAGA	ATTGGGAATC	AACTGTTACA		TGGAATGAAA	CTTCCAGACA
181	GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAAGATT	AGCAATTAAAG	CTCTAAGCCA
241	TCCGAAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG
301	TTGGAGTTG	CTTCGGTCT	GGTCGCTT	GAAGCTCGAA	TTAAAACGCG	ATATTGAAAG
361	TCTTCGGGC	TTCCCTTAA	TCTTTTGAT	GCAATCCGCT	TTGCTCTGA	CTATAATAGT
421	CAGGGTAAAG	ACCTGATTTT	TGATTATG	TCATTCTCGT	TTTCTGAAC	GTTAAAGCA
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT
541	AAACATTITA	CTATTACCCC	CTCTGGCAA	ACTTCTTTG	CAAAGCCTC	TCGCTATTT
601	GGTTTTATC	GTGCGTCTGGT	AAACGAGG	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT
661	AATTCC	GGCGTTATGT	ATCTGCATTA	GTTGAATG	GTATTCTAA	ATCTCAACTG
721	ATGAATCTT	CTACCTGTAA	TAATGTTGTT	CGGTTAGTTC	TTTTTATTAA	CGTAGATT
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGT
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTG	TTACGTTGAT	TTGGGTAATG
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCTGGTC
1021	TGTACACC	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC
1081	GTCTGCGCCT	CGTTCGGCT	AAGTAACATG	GAGCAGGTG	CGGATTTCGA	CACAATTAT
1141	CAGGCGATGA	TACAAATCTC	CGTTGACTT	TGTTTCGCG	TTGGTATAAT	CGCTGGGGT
1201	CAAAGATGAG	TGTTTTAGTG	TATTCTTCG	CCTCTTCG	TTAGGTTGG	TGCCCTCGTA
1261	GTGGCATTAC	GTATTTTAC	CGTTTAATGG	AAACTCCTC	ATGAAAAGT	CTTAGTCCT
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCCTCG	TCCGATGCTG	TCTTCGCTG	CTGAGGGTGA
1381	CGATCCC	AAAGCGGC	TTAACCTCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA
1441	TGGTGGGGC	ATGGTTGTTG	TCATTGTCGG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTT	GGAGCCTTT
1561	TTTTGGAGA	TTTCAACGT	AAAAAAATT	TTATTGCAA	TTCCCTTAGT	TGTTCC
1621	TATTCTCACA	GTGCACAGTC	TGCGTGACG	CAGCCGCCT	CAGTGTCTGG	GGCCCCAGGG
1681	CAGAGGTCA	CCATCTCCTG	CACTGGGAGC	AGCTCCAACA	TCGGGGCAGG	TTATGATGTA
1741	CACTGGTACC	AGCAGCTTCC	AGGAACAGCC	CCCAAAC	TCATCTATGG	TAACAGCAAT
1801	CGGCCCTCAG	GGGTCCCTGA	CCGATTCTCT	GGCTCCAAGT	CTGGCACCTC	AGCCTCCCTG
1861	GCCATCACTG	GGCTCCAGGC	TGAGGATGAG	GCTGATTATT	ACTGCCAGTC	CTATGACAGC
1921	AGCCTGAGTG	GCCTTATGT	CTTCGGA	GGGACCAAGG	TCACCGTC	AGTCAGCCC
1981	AAGGCCAACC	CCACTGTCAC	TCTGTTCCCG	CCCTCCTCTG	AGGAGCTCA	AGCCAACAAG
2041	GCCACACTAG	TGTGCTGAT	CAGTGA	TACCCGGGAG	CTGTGACAGT	GGCCTGGAAG
2101	GCAGATAGCA	GCCCCGTCAA	GGCGGGAGTG	GAGACCACCA	CACCC	ACAAAGCAAC
2161	AAACAAGTACG	CGGCCAGCAG	CTATCTGAGC	CTGACGCC	AGCAGTGGAA	GTCCCACAGA
2221	AGCTACAGCT	GCCAGGTCA	GCATGAAGGG	AGCACCGT	AGAAGACAGT	GGCCCCTACA
2281	GAATGTTCAT	AATAAACCGC	CTCCACCGGG	CGGCCAATT	CTATTCAAG	GAGACAGTC
2341	TAATGAAATA	CCTATTG	ACGGCAGCCG	CTGGATTGTT	ATTACTCGCG	GCCAGCCGG
2401	CCATGGCCGA	AGTTCAATTG	TTAGAGTCTG	GTGGCGGTCT	TGTTCA	GGTGGTTCTT
2461	TACGTCTTC	TTGCGCTGCT	TCCGGATTCA	CTTCTCTTC	GTACGCTATG	TCTGGGTT
2521	GCCAAGCTCC	TGGTAAAGGT	TTGGAGTGGG	TTCTGCTAT	CTCTGGTTCT	GGTGGCAGTA
2581	CTTACTATGC	TGACTCCGTT	AAAGGT	TCACTATCTC	TAGAGACAA	TCTAAGAATA
2641	CTCTCTACTT	GCAGATGAAC	AGCTTAAGGG	CTGAGGACAC	TGCAGTCTAC	TATTGCGCTA
2701	AAGACTATGA	AGGTACTGGT	TATGCTT	ACATATGGGG	TCAAGGTACT	ATGTCACCG
2761	TCTCTAGTGC	CTCCACCAAG	GGCCC	TCTTCCCCCT	GGCACCC	TCCAAGAGCA
2821	CCTCTGGGGG	CACAGCGGCC	CTGGGCTGCC	TGGTCAAGGA	CTACT	GAACCGGTGA
2881	CGGTGTCGTG	GAACTCAGGC	GCCCTGACCA	GGGGCGTCCA	CACCT	GCTGTCCTAC
2941	AGTCTAGCGG	ACTCTACTCC	CTCAGCAGCG	TAGTGACCGT	GCCCT	AGCTTGGGCA
3001	CCCAGACCTA	CATCTGCAAC	GTGAATCACA	AGCCCAGCAA	CACCAAGGTG	GACAAGAAAG

3061 TTGAGCCCAA ATCTTGTGCG GCCGCTCATC ACCACCATCA TCACTCTGCT GAACAAAAAC
 3121 TCATCTCAGA AGAGGATCTG AATGGTGCCG CAGATATCAA CGATGATCGT ATGGCTGGCG
 3181 CCGCTGAAAC TGTTGAAAGT TGTTTAGCAA AACCCCATAC AGAAAATTCA TTTACTAACG
 3241 TCTGGAAAGA CGACAAAACT TTAGATCGTT ACGCTAACTA TGAGGGTTGT CTGTTGAAATG
 3301 CTACAGGCGT TGTAGTTGT ACTGGTGACG AAACTCAGTG TTACGGTACA TGGGTTCTA
 3361 TTGGGCTTGC TATCCCTGAA AATGAGGGTG GTGGCTCTGA GGGTGGCGGT TCTGAGGGTG
 3421 GCGGTTCTGA GGGTGGCGGT ACTAACACCTC CTGAGTACGG TGATACACCT ATTCCGGGCT
 3481 ATACTTATAT CAACCCTCTC GACGGCACTT ATCCGCTGG TACTGAGCAA AACCCGCTA
 3541 ATCCTAATCC TTCTCTTGAG GAGTCTCAGC CTCTTAATAC TTTCATGTTT CAGAATAATA
 3601 GGTTCGAAA TAGGCAGGGG GCATTAACGT TTTATACGGG CACTGTTACT CAAGGCACGT
 3661 ACCCCGTTAA AACTTATTAC CAGTACACTC CTGTATCATC AAAAGCCATG TATGACGCTT
 3721 ACTGGAACGG TAAATTCAAGA GACTGCGCTT TCCATTCTGG CTTTAATGAA GATCCATTG
 3781 TTTGTGAATA TCAAGGCCAA TCGTCTGACC TGCCCTCAACC TCCTGTCAAT GCTGGCGGGCG
 3841 GCTCTGGTGG TGTTCTGGT GGCGGCTCTG AGGGTGGTGG CTCTGAGGGT GGCGGTTCTG
 3901 AGGGTGGCGG CTCTGAGGGG GGCGGTTCCG GTGGTGGCTC TGTTTCCGGT GATTTGATT
 3961 ATGAAAAGAT GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC
 4021 TACAGTCTGA CGCTAAAGGC AAACCTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG
 4081 ATGGTTTCAT TGTTGACGTT TCCGGCCTTG CTAATGGTAA TGTTGCTACT GGTGATTTG
 4141 CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTACACT TTAATGAATA
 4201 ATTTCCGTCA ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA
 4261 GCGCTGGTAA ACCATATGAA TTTCTATTG ATTGTACAA AATAAACTTA TTCCGTGGT
 4321 TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAAC
 4381 TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTG GGTATCCGT TATTATTGCG
 4441 TTTCCTCGGT TTCCCTCTGG TAACTTGTG CCGCTATCTG CTTACTTTTC TTAAAAAGGG
 4501 CTCGGTAAG ATAGCTATTG CTATTTCATT GTTTCTGCT CTTATTATTG GGCTTAAC
 4561 AATTCTTGTG GTTATCTCT CTGATATTAG CGCTCAATTAA CCCTCTGACT TTGTTCA
 4621 TGTTCAGTTA ATTCTCCCGT CTAATGCGCT TCCCTGTTT TATGTTATTC TCTCTGTA
 4681 GGCTGCTATT TTCATTTTG ACGTTAAACA AAAAATCGTT CTTTATTG ATTGGGATA
 4741 ATAATATGGC TGTTTATTT GTAACTGGCA AATTAGGCTC TGAAAGACG CTCGTTAGCG
 4801 TTGGTAAGAT TCAGGATAAA ATTGTAGCTG GGTGAAAAT AGCAACTAAT CTTGATTAA
 4861 GGCTTCAAA CCTCCCGCAA GTCGGGAGGT TCGCTAAAC GCCTCGCGTT CTTAGAATAC
 4921 CGGATAAGGC TTCTATATCT GATTTGCTTG CTATTGGCG CGGTAAATGAT TCCCTACGATG
 4981 AAAATAAAA CGGCTTGCTT GTTCTCGATG AGTGCAGGTAC TTGGTTTAAT ACCCGTTCTT
 5041 GGAATGATAA GGAAAGACAG CCGATTATTG ATTGGTTCT ACATGCTCGT AAATTAGGAT
 5101 GGGATATTAT TTTCTTGTT CAGGACTTAT CTATTGTTGA TAAACAGGGC CGTTCTGCAT
 5161 TAGCTGAACA TGTTGTTAT TGTCGTC TGGACAGAAT TACTTTACCT TTTGTCGGTA
 5221 CTTTATATTTC TCTTATTACT GGCTCGAAA TGCCCTCTGCC TAAATTACAT GTTGGCGTTG
 5281 TAAATATGG CGATTCTCAA TTAAGCCCTA CTGTTGAGCG TTGGCTTTAT ACTGGTAAGA
 5341 ATTTGTATAA CGCATATGAT ACTAAACAGG CTTTTCTAG TAATTATGAT TCCGGTGT
 5401 ATTCTTATTTC AACGCCTTAT TTATCACACG GTGGTATT CAAACCATTA AATTAGGTC
 5461 AGAAAGATGAA ATTAACCTAA ATATATTGA AAAAGTTTC TCGCGTTCTT TGTCTGCGA
 5521 TTGGATTGTC ATCAGCATT ACATATAGTT ATATAACCCA ACCTAAGCCG GAGGTTAAA
 5581 AGGTAGTCTC TCAGACCTAT GATTTGATA AATTCACTAT TGACTCTCT CAGCGCT
 5641 ATCTAAGCTA TCGCTATGTT TTCAAGGATT CTAAGGGAAA ATTAATTAAT AGGGACGATT
 5701 TACAGAAGCA AGGTTATTCA CTCACATATA TTGATTATG TACTGTTTCC ATTAAAAAAG
 5761 GTAATTCAA TGAAATTGTT AAATGTAATT AATTGTTTT TCTTGATGTT TGTTTCATCA
 5821 TCTTCTTTG CTCAGGTAAT TGAAATGAAT AATTGCCCTC TGCGCGATT TGTAACCTGG
 5881 TATTCAAAGC AATCAGGCGA ATCCGTTATT GTTCTCCCG ATGTAAGG TACTGTTACT
 5941 GTATATTCTAT CTGACGTTAA ACCTGAAAAT CTACGCAATT TCTTATTTC TGTTTACGT
 6001 GCTAATAATT TTGATATGGT TGTTCAATT CCTTCCATAA TTCAGAAGTA TAATCCAAAC
 6061 AATCAGGATT ATATTGATGA ATTGCCATCA TCTGATAATC AGGAATATGA TGATAATTCC
 6121 GCTCCTTCTG GTGGTTCTT TGTTCCGAA AATGATAATG TTACTCAAAC TTTAAAATT
 6181 AATAACGTTG GGGCAAAGGA TTTAATACGA GTTGTCAAT TGTTGTAAG GTCTAATACT
 6241 TCTAAATCCT CAAATGTATT ATCTATTGAC GGCTCTAAC TATTAGTTGT TTCTGCACCT
 6301 AAAGATATTG TAGATAACCT TCCTCAATT CTTTCTACTG TTGATTGCCC AACTGACCA
 6361 ATATTGATTG AGGGTTGAT ATTTGAGGTT CAGCAAGGTG ATGCTTAAAGA TTTTCATTT
 6421 GCTGCTGGCT CTCAGCGTGG CACTGTTGCA GGCGGTGTTA ATACTGACCG CCTCACCTCT
 6481 GTTTATCTT CTGCTGGTGG TTGCTCGGT ATTTTAATG GCGATGTTT AGGGCTATCA

6541 GTTCGCGCAT TAAAGACTAA TAGCCATTCA AAAATATTGT CTGTGCCACG TATTCTTACG
 6601 CTTTCAGGTC AGAAGGGTTC TATCTCTGTT GGCCAGAATG TCCCTTTAT TACTGGTCGT
 6661 GTGACTGGTG AATCTGCCAA TGTAATAAT CCATTTCAGA CGATTGAGCG TCAAAATGTA
 6721 GGTATTCCA TGAGCGTTT TCCTGTTGCA ATGGCTGGCG GTAATATTGT TCTGGATATT
 6781 ACCAGCAAGG CCGATAGTTT GAGTTCTTCT ACTCAGGCAA GTGATGTTAT TACTAATCAA
 6841 AGAAAGTATTG CTACAACGGT TAATTGCGT GATGGACAGA CTCTTTACT CGGTGGCCTC
 6901 ACTGATTATA AAAACACTTC TCAAGATTCT GGCGTACCGT TCCTGTCTAA AATCCCTTA
 6961 ATCGGCCTCC TGTTAGCTC CCGCTCTGAT TCCAACGGG AAAGCACGTT ATACGTGCTC
 7021 GTCAAAGCAA CCATAGTACG CGCCCTGTAG CGCGCATTAA AGCGCGGGGG GTGTGGGTGG
 7081 TACGCGCAGC GTGACCGCTA CACTTGCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
 7141 CCCTTCCTTT CTGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC
 7201 TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG ATTGGGTGA
 7261 TGGTCACGT AGTGGGCCAT CGCCCTGTATA GACGGTTTT CGCCCTTGA CGTGGAGTC
 7321 CACGTTCTT AATAGTGGAC TCTTGTCCA AACTGGAACA ACACCTAACCT CTATCTCGGG
 7381 CTATTCTTT GATTTATAAG GGATTGGC GATTTGGAA CCACCATCAA ACAGGATTTT
 7441 CGCCTGCTGG GGCAAACCAAG CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG
 7501 AAGGGCAATC AGCTGTTGCC CGTCTCACTG GTGAAAAGAA AAACCAACCT GGATCCAAGC
 7561 TTGCAGGTGG CACTTTCGG GGAAATGTGC GCGGAACCCC TATTTGTTA TTTTCTAAA
 7621 TACATTCAAA TATGTATCCG CTCATGAGAC AATAACCCCTG ATAAATGCTT CAATAATATT
 7681 GAAAAGGAA GAGTATGAGT ATTCAACATT TCCGTGTCGC CCTTATTCCC TTTTTGCGG
 7741 CATTTCGCCT TCCTGTTTT GCTCACCCAG AAACGCTGGT GAAAGTAAA GATGCTGAAG
 7801 ATCAGTTGGG CGCACGAGTG GGTTACATCG AACTGGATCT CAACAGCGGT AAGATCCTTG
 7861 AGAGTTTCG CCCCGAAGAA CGTTTCCAA TGATGAGCAC TTTAAAGTT CTGCTATGTC
 7921 ATACACTATT ATCCCGTATT GACGCCGGC AAGAGCAACT CGGTGCCGG GCGGGTATT
 7981 CTCAGAATGA CTTGGTTGAG TACTCACCAAG TCACAGAAAA GCATCTTACG GATGGCATGA
 8041 CAGTAAGAGA ATTATGCAGT GCTGCCATAA CCATGAGTGA TAACACTGCG GCCAACTTAC
 8101 TTCTGACAAC GATCGGAGGA CCGAAGGAGC TAACCGCTT TTTGCACAAC ATGGGGGATC
 8161 ATGTAACTCG CCTTGATCGT TGGGAACCGG AGCTGAATGA AGCCATACCA AACGACGAGC
 8221 GTGACACCAC GATGCCTGTA GCAATGCCAA CAACGTTGCG CAAACTATTA ACTGGCGAAC
 8281 TACTTACTCT AGCTTCCCGG CAACAATTAA TAGACTGGAT GGAGGCGGAT AAAGTTGCAG
 8341 GACCACTTCT GCGCTCGGCC CTTCCGGCTG GCTGGTTAT TGCTGATAAA TCTGGAGCCG
 8401 GTGAGCGTGG GTCTCGCGGT ATCATTGCAAG CACTGGGGCC AGATGGTAAG CCCTCCCGTA
 8461 TCGTAGTTAT CTACACGACG GGGAGTCAGG CAACTATGGA TGAACGAAAT AGACAGATCG
 8521 CTGAGATAGG TGCCTCACTG ATTAAGCATT GGTAACTGTC AGACCAAGTT TACTCATATA
 8581 TACTTTAGAT TGATTAAAAA CTTCTTTT AATTAAAAAG GATCTAGGTG AAGATCCTTT
 8641 TTGATAATCT CATGACCAAA ATCCCTTAAC GTGAGTTTC GTTCCACTGT ACGTAAGACC
 8701 CCCAAGCTTG TCGACTGAAT GGCGAATGGC GCTTTGCCTG GTTCCGGCA CCAGAAGCGG
 8761 TGCCGGAAAG CTGGCTGGAG TGCGATCTTC CTGAGGCCGA TACTGTCGTC GTCCCCTCAA
 8821 ACTGGCAGAT GCACGGTTAC GATGCCCA TCTACACCAA CGTAACCTAT CCCATTACGG
 8881 TCAATCCGCC GTTGTTCCTC ACGGAGAAC CGACGGGTTG TTACTCGCTC ACATTAAATG
 8941 TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTGATGGC GTTCCATTG
 9001 GTAAAAAAAT GAGCTGATT AACAAAAATT TAACGCAAT TTTAACAAA TATTAACGTT
 9061 TACAATTAA ATATTGCTT ATACAATCTT CCTGTTTTG GGGCTTTCT GATTATCAAC
 9121 CGGGGTACAT ATGATTGACA TGCTAGTTT ACGATTACCG TTCACTCGATT CTCTTGTGTTG
 9181 CTCCAGACTC TCAGGCAATG ACCTGATAGC CTTTGTAGAT CTCTCAAAAA TAGCTACCCCT
 9241 CTCCGGCATG AATTATCAG CTAGAACGGT TGAATATCAT ATTGATGGTG ATTTGACTGT
 9301 CTCCGGCCTT TCTCACCCCTT TTGAATCTT ACCTACACAT TACTCAGGCA TTGCATTAA
 9361 AATATATGAG GGTTCTAAA ATTTTATCC TTGCGTTGAA ATAAAGGCTT CTCCCGCAAA
 9421 AGTATTACAG GGTCTATAATG TTTTGGTAC AACCGATTTA GCTTATGCT CTGAGGCTTT
 9481 ATTGCTTAAT TTTGCTAATT CTTTGCTTGC CCTGTATGAT TTATTGGATG TT

Please delete Table 22 and replace it with the following table:

Table 22: Primers used in RACE amplification:

Heavy chain	
HuC μ -FOR (1st PCR)	5'-TGG AAG AGG CAC GTT CTT TTC TTT-3' <u>(SEQ ID NO: 457)</u>
HuC μ -Nested (2nd PCR)	5' CTT TTC TTT GTT GCC GTT GGG GTG-3' <u>(SEQ ID NO: 458)</u>
Kappa light chain	
HuCkFor (1st PCR)	5'-ACA CTC TCC CCT GTT GAA GCT CTT-3' <u>(SEQ ID NO: 459)</u>
HuCkForAsCI (2nd PCR)	5'-ACC GCC TCC ACC GGG CGC GCC TTA TTA ACA CTC TCC CCT GTT GAA GCT CTT-3' <u>(SEQ ID NO: 460)</u>
Lambda light chain	
HuCLambdaFor (1st PCR)	5'-TGA ACA TTC TGT AGG GGC CAC TG-3' <u>(SEQ ID NO: 461)</u>
HuCL2-FOR	5'-ACA GCA TTC TGC AGG GGC CAC TG-3' <u>(SEQ ID NO: 462)</u>
HuCL7-FOR	
HuCLambdaForAsCI (2nd PCR)	
HuCL2-FOR-ASC	5'-ACC GCC TCC ACC GGG CGC GCC TTA TGA ACA TTC TGT AGG GGC CAC TG-3' <u>(SEQ ID NO: 463)</u>
HuCL7-FOR-ASC	5'-ACC GCC TCC ACC GGG CGC GCC TTA TTA AGA GCA TTC TGC AGG GGC CAC TG-3' <u>(SEQ ID NO: 464)</u>
GeneRacer 5'	Primers provided with the kit (Invitrogen)
5'A 1st PCR	5' CGACTGGAGCACGAGCACACTGA 3' <u>(SEQ ID NO: 465)</u>
5'NA 2nd PCR	5' GGACACTGACATGGACTGAAGGAGTA-3' <u>(SEQ ID NO: 466)</u>

Please delete Table 23 and replace it with the following table:

Table 23: ONS used in Capture of kappa light chains using CJ method and *BsMAI*

All ONS are written 5' to 3'.

REadapters (6)
 ON_20SK15012 (SEQ ID NO: 467)
 ON_20SK15112 (SEQ ID NO: 468)
 ON_20SK15A17 (SEQ ID NO: 469)
 ON_20SK15A27 (SEQ ID NO: 470)
 ON_20SK15A11 (SEQ ID NO: 471)
 ON_20SK15B3 (residues 1-20 of SEQ ID NO: 477)

Bridges (6)

kapbri1012	999AGGATGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 472)
kapbri1112	999AAGATGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 473)
kapbri1A17	999AGGATGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 474)
kapbri1A27	999TGCCTGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 475)
kapbri1A11	999TGGGTGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 476)
kapbri1B3	999AGTCTGGAGACTGGGTCAATCTGGATGTCCTTGTGCACTGTGACAGGG	(SEQ ID NO: 477)

Extender (5' biotinylated)
 kapext1biot ccttttttccAACTTggc

Primers
 kapPCR1 ccTcTgtcAcAGtgcACAAgAc (SEQ ID NO: 479)
 kapfor 5' -aca ctc tcc cct gtt gaa gct ctt-3' (SEQ ID NO: 480)

Please delete Table 25 and replace it with the following table:

Table 25: h3401-h2 captured Via CJ with BsmAI

(Nucleotide sequence is SEQ ID NO: 481, Amino acid sequence is SEQ ID NO: 482)

! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! S A Q D I Q M T Q S P A T L S
aGT GCA Caa gac atc cag atg acc cag tct cca gcc acc ctg tct
! ApaLI... a gcc acc ! L25,L6,L20,L2,L16,A11
! Extender.....Bridge...

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
! V S P G E R A T L S C R A S Q
gtg tct cca ggg gaa agg gcc acc ctc tcc tgc agg gcc agt cag

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! S V S N N L A W Y Q Q K P G Q
agt gtt agt aac aac tta gcc tgg tac cag cag aaa cct ggc cag

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
! V P R L L I Y G A S T R A T D
gtt ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act gat

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! I P A R F S G S G S G T D F T
atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac ttc act

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! L T I S R L E P E D F A V Y Y
ctc acc atc agc aga ctg gag cct gaa gat ttt gca gtg tat tac

! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! C Q R Y G S S P G W T F G Q G
tgt cag cgg tat ggt agc tca ccg ggg tgg acg ttc ggc caa ggg

! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! T K V E I K R T V A A P S V F
acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! I F P P S D E Q L K S G T A S
atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct

! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
! V V C L L N N F Y P R E A K V
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta

! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
! Q W K V D N A L Q S G N S Q E
cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag

```

! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
! S V T E Q D S K D S T Y S L S
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc

! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195

! S T L T L S K A D Y E K H K V
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc

! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
! Y A C E V T H Q G L S S P V T
tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg cct gtc aca

! 211 212 213 214 215 216 217 218 219 220 221 222 223
! K S F N K G E C K G E F A
aag agc ttc aac aaa gga gag tgt aag ggc gaa ttc gc.....

```

Please delete Table 26 and replace it with the following table:

Table 26: h3401-d8 KAPPA captured with CJ and *BsmAI*
(Nucleotide sequence is SEQ ID NO: 484; Amino acid sequence is SEQ ID NO: 485)

```

! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! S A Q D I Q M T Q S P A T L S
aGT GCA Caa gac atc cag atg acc cag tct ect gcc acc ctg tot
! ApaLI...Extender.....a gcc acc ! L25,L6,L20,L2,L16,A11
! A GCC ACC CTG TCT ! L2 (SEQ ID NO: 483)

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
! V S P G E R A T L S C R A S Q
gtg tct cca ggt gaa aga gcc acc ctc tcc tgc agg gcc agt cag
! GTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC ! L2

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! N L L S N L A W Y Q Q K P G Q
aat ctt ctc agc aac tta gcc tgg tac cag cag aaa cct ggc cag

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
! A P R L L I Y G A S T G A I G
gct ccc agg ctc ctc atc tat ggt gct tcc acc ggg gcc att ggt

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! I P A R F S G S G S G T E F T
atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! L T I S S L Q S E D F A V Y F
ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtg tat ttc

! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! C Q Q Y G T S P P T F G G G T
tgt cag cag tat ggt acc tca ccg ccc act ttc ggc gga ggg acc

```

! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 ! K V E I K R T V A A P S V F I
 aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc

 ! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
 ! F P P S D E Q L K S G T A S V
 ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt

 ! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
 ! V C P L N N F Y P R E A K V Q
 gtg tgc ccg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag

 ! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
 ! W K V D N A L Q S G N S Q E S
 tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt

 ! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
 ! V T E Q D N K D S T Y S L S S
 gtc aca gag cag gac aac aag gac agc acc tac agc ctc agc agc

 ! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
 ! T L T L S K V D Y E K H E V Y
 acc ctg acg ctg agc aaa gta gac tac gag aaa cac gaa gtc tac

 ! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
 ! A C E V T H Q G L S S P V T K
 gcc tgc gaa gtc acc cat cag ggc ctt agc tcg ccc gtc acg aag

 ! 211 212 213 214 215 216 217 218 219 220 221 222 223
 ! S F N R G E C K K E F V
 agc ttc aac agg gga gag tgt aag aaa gaa ttc gtt t

Please delete Table 27 and replace it with the following table:

Table 27: V3-23 VH framework with variegated codons shown

! (Nucleotide sequence is SEQ ID NO: 486; Amino acid sequence is SEQ ID NO: 487)

! 17 18 19 20 21 22
 ! A Q P A M A
 5'-ctg tct gaa cG GCC cag ccG GCC atg gcc 29
 3'-gac aga ctt gc cgg gtc ggc cgg tac cgg
 ! Scab.....SfiI.....
 ! NgoMI...
 ! NcoI....
 !
 ! FR1(DP47/V3-23)-----
 ! 23 24 25 26 27 28 29 30
 ! E V Q L L E S G
 gaa|gtt|CAA|TTG|tta|gag|tct|ggt| 53
 ctt|caa|gtt|aac|aat|ctc|aga|cca|
 ! | MfeI |
 !

-----FR1-----
! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! G G L V Q P G G S L R L S C A
! |ggc|ggt|ctt|gtt|cag|cct|ggt|gtt|tct|tta|cgt|ctt|tct|tgc|gct| 98
! |ccg|cca|gaa|caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|
!
! Sites to be varied--> *** *** ***
! ---FR1----->|...CDR1.....|---FR2-----
! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
! A S G F T F S S Y A M S W V R
! |gtc|TCC|GGA|ttc|act|ttc|tct|tCG|TAC|Gct|atg|tct|tgg|gtt|cgC| 143
! |cga|agg|cct|aag|tga|aag|aga|acg|atg|cga|tac|aga|acc|caa|gca|
! | BspEI | | BsiWI | |BstXI.
!
! Sites to be varies--> *** *** ***
! ---FR2----->|...CDR2.....
! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! Q A P G K G L E W V S A I S G
! |CAa|get|ccT|GGt|aaa|ggt|ttg|gag|tgg|gtt|tct|gct|atc|tct|ggt| 188
! |gtt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|cga|tag|aga|cca|
! ...BstXI |
!
! *** ***
!CDR2.....|---FR3---
! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! S G G S T Y Y A D S V K G R F
! |tct|ggt|ggc|agt|act|tac|tat|gtc|gac|tcc|gtt|aaa|ggt|cgC|ttc| 233
! |aga|cca|ccg|tca|tga|atg|ata|cga|ctg|agg|caa|ttt|cca|gca|aag|
!
! -----FR3-----
! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! T I S R D N S K N T L Y L Q M
! |act|atc|TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg| 278
! |tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|
! | XbaI |
!
! -----FR3----->|
! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
! N S L R A E D T A V Y Y C A K
! |aac|agC|TTA|AGg|gtc|gag|gac|aCT|GCA|Gtc|tac|tat|tgc|gct|aaa| 323
! |ttg|tcg|aat|tcc|cga|ctc|ctg|tga|cgt|cag|atg|ata|acg|cga|ttt|
!
! |AflII | | PstI |
!
!CDR3.....|---FR4-----
! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! D Y E G T G Y A F D I W G Q G
! |gac|tat|gaa|ggt|act|ggt|tat|gtc|tta|gac|ATA|TGg|ggt|caa|ggt| 368
! |ctg|ata|ctt|cca|tga|cca|ata|cga|aag|ctg|tat|acc|cca|gtt|cca|
! | NdeI |
!
! -----FR4----->|

```

! 136 137 138 139 140 141 142
! T M V T V S S
|act|atG|GTC|ACC|gtc|tct|agt- 389
! |tga|tac|cag|tgg|cag|aga|tca-
! | BstEII |

!
! 143 144 145 146 147 148 149 150 151 152
! A S T K G P S V F P
gcc tcc acc aaG GGC CCa tcg GTC TTC ccc-3' 419
! cgg agg tgg ttc ccc ggt agc cag aag ggg-5'
! Bsp120I. BbsI...(2/2)
! ApaI....

```

(SFPRMET) 5'-ctg tct gaa cG GCC cag ccG-3' (SEQ ID NO: 488)
 (TOPFR1A) 5'-ctg tct gaa cG GCC cag ccG GCC atg gcc-
 gaa|gtt|CAA|TTG|tta|gag|tct|ggg|-
 |ggc|ggg|ctt|gtt|cag|cct|ggg|tct|tta-3' (SEQ ID NO: 489)
 (BOTFR1B) 3'-caa|gtc|gga|cca|cca|aga|aat|gca|gaa|aga|acg|cga|-
 |cga|agg|cct|aag|tga|aag-5' ! bottom strand (SEQ ID NO: 490)
 (BOTFR2) 3'-acc|caa|gca|-
 |gtt|cga|gga|cca|ttt|cca|aac|ctc|acc|caa|aga|-5' ! bottom strand (SEQ ID NO: 491)
 (BOTFR3) 3'- a|cga|ctg|agg|caa|ttt|cca|gca|aag|-
 |tga|tag|aga|tct|ctg|ttg|aga|ttc|tta|tga|gag|atg|aac|gtc|tac|-
 |ttg|tgc|aat|tcc|cga|etc|ctg|tga-5' (SEQ ID NO: 492)
 (F06) 5'-gC|TTA|AGg|gct|gag|gac|act|GCA|Gtc|tac|tat|tgc|gct|aaa|-
 |gac|tat|gaa|ggg|act|ggg|tat|gct|ttc|gaC|ATA|TGg|ggg|c-3' (SEQ ID NO: 493)
 (BOTFR4) 3'-cga|aag|ctg|tat|acc|cca|gtt|cca|-
 |tga|tac|cag|tgg|cag|aga|tca-
 egg agg tgg ttc ccc ggt agc cag aag ggg-5' ! bottom strand (SEQ ID NO: 494)
 (BOTPRCPRIM) 3'-gg ttc ccc ggt agc cag aag ggg-5' (SEQ ID NO: 495)

!

! CDR1 diversity

!

(ON-vgC1) 5'-gct|TCC|GGA|ttc|act|ttc|tct|<1>|TAC|<1>|atg|<1>|-
 ! CDR1.....6859
 |tgg|gtt|cgC|CAa|gct|ccT|GG-3' (SEQ ID NO: 496)

!

! <1> stands for an equimolar mix of {ADEFGHIKLMNPQRSTVWY}; no C
 ! (this is not a sequence)

!

! CDR2 diversity

!

(ON-vgC2) 5'-ggg|ttg|gag|tgg|gtt|tct|<2>|atc|<2>|<3>|-
 ! CDR2.....
 |tct|ggg|ggc|<1>|act|<1>|tat|gct|gac|tcc|gtt|aaa|gg-3' (SEQ ID NO: 497)
 ! CDR2.....
 ! <1> is an equimolar mixture of {ADEFGHIKLMNPQRSTVWY}; no C
 ! <2> is an equimolar mixture of {YRWVGS}; no ACDEFHIKLMNPQT
 ! <3> is an equimolar mixture of {PS}; no ACDEFGHIKLMNQRTVWY

Please delete Table 28 and replace it with the following table:

Table 28: Stuffer used in VH (SEQ ID NO: 498)

1 TCCGGAGCTT CAGATCTGTT TGCCCTTTTG TGCGGGTGGTG CAGATCGCGT TACGGAGATC
61 GACCGACTGC TTGAGCAAAA GCCACCGCTTA ACTGCTGATC AGGCATGGGA TGTTATTTCGC
121 CAAACAGTC GTCAAGGATCT TAACCTGAGG CTTTTTAC CTACTCTGCA AGCAGGGACA
181 TCTGGTTTCA CACAGAGCGA TCCGGCTCGT CAGTTGGTAG AAACATTAAC ACGTTGGGAT
241 GGCACTCAATT TGCTTAATGA TGATGGTAAA ACCTGGCAGC AGCCAGGCTC TGCCATCCTG
301 AACGTTTGGC TGACCAAGTAT GTTGAAGCGT ACCGTAAGTGG CTGCCGTACC TATGCCATT
361 GATAAGTGGT ACAGGCCAG TGGCTACGAA ACAACCCAGG AGGGCCCCAAC TGGITTCGCTG
421 AATAAAGTG TTGGAGCAAA AATTITGTAT GAGGGGGTGC AGGGAGACAA ATCCAATC
481 CCACAGGGGG TTGATCTGTT TGCTGGAAA CCACAGCAGG AGGTTGTGTT GGCTGGCTG
541 GAAGATACT GGGAGACTCT TTCCAAACGC TATGGCAATA ATGTGAGTAA CTGGAAAACA
601 CCTGCAATGG CCTTAACGTT CGGGCAAAAT AATTCTTGT GTGTACCGCA GGCCGGAGCG
661 GAAGAAACGC GTCATCAGGC GGAGTATCAA AACCGTGGAA CAGAAAACGA TATGATTGTT
721 TTCTCACCAA CGACAAAGCGA TCGTCCGTG CTGCCCCGG ATGTGGTCGC ACCGGGTCA
781 AGTGGGTTA TTGCTCCCGA TGGAACAGTT GATAAGCAGTCA GCTGAAAATG
841 TACGAAAATT TTGGCCGTAA GTCGCTGG TAACGAAGC AGGATGTGGA GGCGCATAAG
901 GAGTCGTCTA GA

Please delete Table 29 and replace it with the following table:

Table 29: DNA sequence of pCES5

! pCES5 6680 bases = pCes4 with stuffers in CDR1-2 and CDR3 2000.12.13
!
! Ngene = 6680
! Useful REs (cut MAnoLI fewer than 3 times) 2000.06.05
!
! Non-cutters
!Acc65I Ggtacc AfeI AGCgct AvrII Cctagg
!BsaBI GATNNnnatc BsiWI Cgtacg BsmFI Nnnnnnnnnnnnnngtccc
(SEQ ID NO: 499)
!BsrGI Tgtaca BstAPI GCANNNNntgc BstBI Ttcgaa
(SEQ ID NO: 501)
!BstZ17I GTAtac BtrI CACgtg Ecl136I GAGctc
!EcoRV GATatc FseI GGCGGGcc KpnI GGTACc
!MscI TGGccca NruI TCGcga NsiI ATGCAt
!PacI TTAATtaa PmeI GTTTaaac PmlI CACgtg
!PpuMI RGgwccy PshAI GACNNnnngtc SacI GAGCTc
(SEQ ID NO: 502)
!SacII CCGCgg SbfI CCTGCAgg SexAI Accwgg
!SgfI GCGATcgc SnaBI TACgtt SpeI Actagt
!SphI GCATGc Sse8387I CCTGCAgg StuI AGGect
!SwaI ATTtaat XmaI Cccggg
!
! cutters
! Enzymes that cut more than 3 times.
!AlwNI CAGNNNctg 5
!BsgI ctgcac 4
!BsrFI Rccggy 5
!EarI CTCTTCNnnn 4
(SEQ ID NO: 625)
!FauI nNNNNNNNGCGGG 10
! **(SEQ ID NO: 503)**
! Enzymes that cut from 1 to 3 times.
!
!EcoO109I RGgnccy 3 7 2636 4208
!BssSI Ctcgtg 1 12
!-"- Cacgag 1 1703
!BspHI Tcatga 3 43 148 1156
!AatII GACGTc 1 65
!BciVI GTATCCNNNNNN 2 140 1667
(SEQ ID NO: 504)
!Eco57I CTGAAG 1 301
!-"- cttcag 2 1349
!AvaI Cycgrg 3 319 2347 6137
!BsiHKAI GWGCWc 3 401 2321 4245
!HgiAI GWGCWc 3 401 2321 4245
!BcgI gcannnnnntcg 1 461
(SEQ ID NO: 505)

!ScaI AGTact	1	505
!PvuI CGATcg	3	616 3598 5926
!FspI TGCgca	2	763 5946
!BglI GCCNNNNnggc	3	864 2771 5952
<u>(SEQ ID NO: 506)</u>		
!BpmI CTGGAG	1	898
!-"- ctccag	1	4413
!BsaI GGTCTCNnnnn	1	916
<u>(SEQ ID NO: 507)</u>		
!AhdI GACNNNNnngtc	1	983
<u>(SEQ ID NO: 508)</u>		
!Eam1105I GACNNNNnngtc	1	983
<u>(SEQ ID NO: 509)</u>		
!DrdI GACNNNNnngtc	3	1768 6197 6579
<u>(SEQ ID NO: 510)</u>		
!SapI gaagagc	1	1998
!PvuII CAGctg	3	2054 3689 5896
!PflMI CCANNNNntgg	3	2233 3943 3991
<u>(SEQ ID NO: 511)</u>		
!HindIII Aagctt	1	2235
!ApaLI Gtgcac	1	2321
!BspMI Nnnnnnnnnngcaggt	1	2328
<u>(SEQ ID NO: 512)</u>		
!-"- ACCTGCNNNNn	2	3460
<u>(SEQ ID NO: 513)</u>		
!PstI CTGCAg	1	2335
!AccI GTmkac	2	2341 2611
!HincII GTYrac	2	2341 3730
!SalI Gtgcac	1	2341
!TliI Ctcgag	1	2347
!XhoI Ctcgag	1	2347
!BbsI gtctc	2	2383 4219
!BpI GCtnagc	1	2580
!EspI GCtnagc	1	2580
!SgrAI CRccgggyg	1	2648
!AgeI Accgggt	2	2649 4302
!AscI GGcgcgcc	1	2689
!BssHII Gcgcgc	1	2690
!SfiI GGCCNNNNnggcc	1	2770
<u>(SEQ ID NO: 514)</u>		
!NaeI GCCggc	2	2776 6349
!NgoMIV Gccggc	2	2776 6349
!BtgI Ccrrygg	3	2781 3553 5712
!DsaI Ccrrygg	3	2781 3553 5712
!NcoI Ccatgg	1	2781
!StyI Ccwwgg	3	2781 4205 4472
!MfeI Caattg	1	2795
!BspEI Tccgga	1	2861
!BglIII Agatct	1	2872
!BclI Tgatca	1	2956
!Bsu36I CCtnagg	3	3004 4143 4373
!XcmI CCANNNNNnnnntgg	1	3215
<u>(SEQ ID NO: 515)</u>		

!MluI Acgcgt	1 3527
!HpaI GTTaac	1 3730
!XbaI Tetaga	1 3767
!	
!AflII Cttaag	1 3811
!BsmI NGcattc	1 3821
!-"- GAATGCN	1 4695
!RsrII CGgwccg	1 3827
!NheI Gctagc	1 4166
!BstEII Ggttnacc	1 4182
!BsmBI CGTCTCNnnnn	2 4188 6625
<u>(SEQ ID NO: 516)</u>	
!-"- Nnnnnngagacg	1 6673
<u>(SEQ ID NO: 517)</u>	
!ApaI GGGCCc	1 4209
!BanII GRGCYc	3 4209 4492 6319
!Bsp120I Gggccc	1 4209
!PspOMI Gggccc	1 4209
!BseRI NNnnnnnnnnnctcctc	1 4226
<u>(SEQ ID NO: 518)</u>	
!-"- GAGGAGNNNNNNNNNNNN	1 4957
<u>(SEQ ID NO: 519)</u>	
!EcoNI CCTNNnnnagg	1 4278
<u>(SEQ ID NO: 520)</u>	
!PflFI GACNnngtc	1 4308
!Tth111I GACNnngtc	1 4308
!KasI Ggcgcc	2 4327 5967
!BstXI CCANNNNNntgg	1 4415
<u>(SEQ ID NO: 521)</u>	
!NotI GCggccgc	1 4507
!EagI Cggccg	1 4508
!BamHI Ggatcc	1 5169
!BspDI ATcgat	1 5476
!NdeI CAtatg	1 5672
!EcoRI Gaattc	1 5806
!PsiI TTAtaa	1 6118
!DraIII CACNNNgtg	1 6243
!BsaAI YACgtr	1 6246
!	

(Nucleotide sequence is SEQ ID NO: 522 and Amino acid sequence is SEQ ID NO: 523, respectively)

1 gacgaaaggg cCTCGTGata cgcctatttt tataggttaa tgtcatgata ataatggttt
! BssSI.(1/2)
61 cttAGACGTC aggtggcaact ttccggggaa atgtgcgcgg aaccctattt tgtttatttt
! AatII.
121 tctaaataca ttcaaataatG TATCCgctca tgagacaata accctgataa atgcttcaat
! BciVI..(1 of 2)
181 aatattgaaa aaggaagagt
! Base # 201 to 1061 = ApR gene from pUC119 with some RE sites removed
!
! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! fM S I Q H F R V A L I P F F A
201 atg agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg
!

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 ! A F C L P V F A H P E T L V K
 246 gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa
 !
 ! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
 ! V K D A E D Q L G A R V G Y I
 291 gta aaa gat gct gaa gat cag ttg ggt gcc cga gtg ggt tac atc
 !
 ! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
 ! E L D L N S G K I L E S F R P
 336 gaa ctg gat ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc
 !
 ! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
 ! E E R F P M M S T F K V L L C
 381 gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt
 !
 ! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
 ! G A V L S R I D A G Q E Q L G
 426 ggc gcg gta tta tcc cgt att gac gcc ggg caa gaG CAa ctc ggT
 ! BcgI.....
 !
 ! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
 ! R R I H Y S Q N D L V E Y S P
 471 CGc cgc ata cac tat tct cag aat gac ttg gtt gAG TAC Tca cca
 !..BcgI..... ScaI....
 !
 ! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 ! V T E K H L T D G M T V R E L
 516 gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta
 !
 ! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
 ! C S A A I T M S D N T A A N L
 561 tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
 !
 ! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
 ! L L T T I G G P K E L T A F L
 606 ctt ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg
 ! PvuI.... (1/2)
 !
 ! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
 ! H N M G D H V T R L D R W E P
 651 cac aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg
 !
 ! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
 ! E L N E A I P N D E R D T T M
 696 gag ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg
 !
 ! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
 ! P V A M A T T L R K L L T G E
 741 cct gta GCA ATG gca aca acg tTG CGC Aaa cta tta act ggc gaa
 ! BsrDI..(1/2) FspI.... (1/2)
 !
 ! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210

! L L T L A S R Q Q L I D W M E
 ! 786 cta ctt act cta gct tcc cg_g caa caa tta ata gac tgg atg gag
 !
 ! 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
 ! A D K V A G P L L R S A L P A
 ! 831 gcg gat aaa gtt gca gga cca ctt ctg cgc t_{cg} gcc ctt ccg gct
 !
 ! 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
 ! G W F I A D K S G A G E R G S
 ! 876 ggc tgg ttt att gct gat aaa tCT GGA Gcc ggt gag cgt gGG TCT
 ! BpmI....(1/2) BsaI....
 !
 ! 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
 ! R G I I A A L G P D G K P S R
 ! 921 Cgc ggt atC ATT GC_a gca ctg ggg cca gat ggt aag ccc tcc cgt
 ! BsaI..... BsrDI...(2/2)
 !
 ! 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
 ! I V V I Y T T G S Q A T M D E
 ! 966 atc gta gtt atc tac acG AC_g ggg aGT Cag gca act atg gat gaa
 ! AhdI.....
 !
 ! 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285
 ! R N R Q I A E I G A S L I K H
 ! 1011 cga aat aga cag atc gct gag ata ggt gcc tca ctg att aag cat
 !
 ! 286 287
 ! W
 ! 1056 tgg taa
 ! 1062 ctgtcagac caagttact
 ! 1081 catatatact ttagattgat taaaacttc attttaatt taaaaggatc taggtgaaga
 ! 1141 tcctttga taatctatg accaaaatcc cttAACgttgc gtttcgttc cactgagcgt
 ! 1201 cagacccgt agaaaaagatc aaaggatctt ct_{tg}gagatcc tttttctg cgcgtaatct
 ! 1261 gctgcttgca aacaaaaaaaaa ccaccgtac cagcgggtgt ttgttgccg gatcaagagc
 ! 1321 taccaactct tttccgaag gtaactggct tcagcagacg gcagatcca aatactgtcc
 ! 1381 ttctagtgta gccgtagta gcccaccact tcaagaactc t_{gt}gacccg cctacatacc
 ! 1441 tcgctctgtc aatcctgtta ccagtggctg ctgcccagtgg cgataagtgc t_{gt}cttaccg
 ! 1501 ggtggactc aagacgatag ttaccggata aggcgcagcg gtccggctga acgggggggt
 ! 1561 cgtgcataca gcccagctt gaggcgaacga cctacaccga actgagatac ctacagcgtg
 ! 1621 agcattgaga aagcgcacg ctccggaa ggagaaaggc ggacagGTAT CCgttaagcg
 ! BciVI.. (2 of 2)
 ! 1681 gcagggtcgg aacaggagag cgCACGAGgg agctccagg gggaaacgcc tggatctt
 ! BssSI.(2/2)
 ! 1741 atagtccgtt cgggtttcgc caccctgtac ttgagcgtc atttttgtga tgctcgtcag
 ! 1801 gggggcggag cctatggaaa aacgcgcacgc acgcggccctt ttacgggtc ctggcccttt
 ! 1861 gctggccctt tgctcACATG Ttctttctg cgttatcccc tgattctgtg gataaccgt
 ! PciI..
 ! 1921 ttaccgcctt tgagtgagct gataccgc gccgcagccg aacgaccgag cgcagcgt
 ! 1981 cagtgagcga ggaagcgGAA GAGCgcacaa tacgcaaaacc gcctctcccc ggcgcgttggc
 ! SapI....
 ! 2041 cgattcatta atgCAGCTGg cacgacaggt ttccgcactg gaaagcgggc agtgagcga
 ! PvuII.(1/3)
 ! 2101 acgcaatTAA TGTgagttag ctcaactcatt aggcacccca ggcTTTACAC tttatgcctt

```

!      ..-35..      Plac      ..-10.
2161  cggctcgat gttgtgtgga atttgagcg gataacaatt tcacaCAGGA AACAGCTATG
!                                         M13Rev_seq_primer
2221  ACCatgatta cgCCAAGCTT TGGagcctt ttttggaga tttcaac
!                                         PflMI.....
!                                         Hind3.
! signal::linker::CLight
!
!      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
!      fM K K L L F A I P L V V P F Y (Amino acid sequence is SEQ ID NO: 524)
2269  gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat
!
!                                         Linker..... End of FR4
!      16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
!      S H S A Q V Q L Q V D L E I K
2314  tct cac aGT GCA Cag gtc caa CTG CAG GTC GAC CTC GAG atc aaa
!                                         ApaLI..... PstI... XhoI...
!                                         BspMI...
!                                         SalI...
!                                         AccI...(1/2)
!                                         HincII.(1/2)
!
! Vlight domains could be cloned in as ApaLI-XhoI fragments.
! VL-CL(kappa) segments can be cloned in as ApaLI-Ascl fragments. <-----
!
! Ckappa-----
!      31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
!      R G T V A A P S V F I F P P S
2359  cgt gga act gtg gct gca cca tct GTC TTC atc ttc ccg cca tct
!                                         BbsI...(1/2)
!
!      46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
!      D E Q L K S G T A S V V C L L
2404  gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg
!
!      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
!      N N F Y P R E A K V Q W K V D
2449  aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
!
!      76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
!      N A L Q S G N S Q E S V T E Q
2494  aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag
!
!      91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
!      D S K D S T Y S L S S T L T L
2539  gac agc aag gac agc acc tac agc ctc agc agc acc ctg acG CTG
!                                         EspI...
!
!      106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
!      S K A D Y E K H K V Y A C E V
2584  AGC aaa gca gac tac gag aaa cac aaa GTC TAC gcc tgc gaa gtc
! ...EspI.... AccI...(2/2)
!

```

! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
! T H Q G L S S P V T K S F N R
2629 acc cat cag ggc ctg agt tcA CCG GTg aca aag agc ttc aac agg
! AgeI....(1/2)
!
! 136 137 138 139 140
! G E C . .
2674 gga gag tgt taa taa GG CGCGCCaatt
! AscI.....
! BssHII.
!
2701 ctattcaag gagacagtca ta
!
! PelB::3-23(stuffed)::CH1::III fusion gene
!
! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! M K Y L L P T A A A A G L L L L (Amino acid sequence is SEQ ID NO: 525)
2723 atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc
!
!-----
!
! 16 17 18 19 20 21 22
! A A Q P A M A
2768 gcG GCC cag ccG GCC atg gcc
! SfI.....
! NgoMIV..(1/2)
! NcoI....
!
! FR1(DP47/V3-23)-----
! 23 24 25 26 27 28 29 30
! E V Q L L E S G
2789 ga|gtt|CAA|TTG|tta|gag|tct|ggt|
! | MfeI |
!
! -----FR1-----
! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! G G L V Q P G G S L R L S C A
2813 |ggc|ggt|ctt|gtt|cag|cct|ggt|ggt|tct|tta|cgt|ctt|tct|tgc|gct|
!
! ----FR1----
! 46 47 48
! A S G
2858 |gct|TCC|GGA|
! | BspEI |
!
! Stuffer for CDR1, FR2, and CDR2----->
! There are no stop codons in this stuffer.
2867 gcttcAGATC Tgtttgcctt
! BglII..
2887 ttgtgggt ggtgcagatc gcgttacgga gatcgaccga ctgcttgagc aaaagccacg
2947 cttaactgcT GATCAggcat gggatgttat tcgccaaacc agtcgtcagg atcttaacct
! BclI...
3007 gaggctttt ttacctactc tgcaaggcagc gacatctggt ttgacacaga gcgatccgcg

3067 tcgtcagttg gtagaaacat taacacgttg ggtatggcatc aatttgctta atgtatgtgg
 3127 taaaacctgg cagcagccag gctctccat cctgaacgtt tggctgacca gtatgttggaa
 3187 gcgtaccgtt gtggctgccc tacctatgCC Atttgataag TGGtacagcg ccagtggcta
 ! XcmI.....
 3247 cggaaacaacc caggacggcc caactggttc gctgaatata agtgtggag caaaaatttt
 3307 gtatgaggcg gtgcagggag acaaattacc aatcccacag gcggttgatc tggttgctgg
 3367 gaaaccacag caggagggtt tggtggctgc gctggaagat acctgggaga ctcttccaa
 3427 acgtatggc aataatgtga gtaactgaa aacacctgca atggcctaa cgttccgggc
 3487 aaataatttc ttgggtgtac cgcaggccgc agcggaaagaa ACGCGTcatc aggccggagta
 ! MuI..
 3547 tcaaaaccgt ggaacagaaaa acgatatgtat tggttctca ccaacgacaa gcgatcgatcc
 3607 tggtctgccc tggatgtgg tcgcacccgg tcagagtggg ttatgtctt ccgatggaaac
 3667 agttgataag cactatgaag atcagctgaa aatgtacgaa aatttggcc gtaagtgcgt
 ! PvuII.
 3727 ctgGTTAACg aagcaggatg tggaggcgca taaggagtgc
 ! HpaI..
 ! HincII(2/2)
 !
 ! -----FR3-----
 ! 4 5 6 7 8 9 10 11 12 13 14 15 16
 ! 93 94 95 96 97 98 99 100 101 102 103 104 105
 ! S R D N S K N T L Y L Q M **(Amino acid sequence is SEQ ID NO: 526)**
 3767 |TCT|AGA|gac|aac|tct|aag|aat|act|ctc|tac|ttg|cag|atg|
 ! | XbaI |
 !
 ! -----FR3----->|
 ! 17 18 19 20
 ! 106 107 108 109
 ! N S L s l s i r s g
 3806 |aac|agC|TTA|AG t ctg agc att CGG TCC G
 ! |AflIII | RsrII..
 !
 ! q h s p nt .
 3834 gg caa cat tct cca aac tga ccagacga cacaacggc
 3872 ttacgctaaa tcccgccat gggatggtaa agaggtggcg tctttgctgg cctggactca
 3932 tcagatgaag gccaaaaatt ggcaggagggt gacacagcag gcagcgaaac aagcactgac
 3992 catcaactgg tactatgctg atgtaaacgg caatattggt tatgttccata ctgggtctta
 4052 tccagatcgt caatcaggcc atgatccggc attaccgtt cctgttacgg gaaaatggga
 4112 ctggaaagggtt ctattgcctt ttgaaatgaa ccctaaggtt tataaccccc ag
 4164 aa GCTAGC ctgcggcttc
 ! NheI..
 !
 4182 G|GTC|ACC| gtc tca agc
 ! | BstEII |
 !
 ! **(Amino acid sequence is SEQ ID NO: 527)**
 ! 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
 ! A S T K G P S V F P L A P S S
 4198 gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc
 !
 ! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
 ! K S T S G G T A A L G C L V K
 4243 aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag

!
! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
! D Y F P E P V T V S W N S G A
4288 gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc
!
! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
! L T S G V H T F P A V L Q S S
4333 ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tcc tca
!
! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
! G L Y S L S S V V T V P S S S
4378 gga ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc agc agc
!
! 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
! L G T Q T Y I C N V N H K P S
4423 ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc
!
! 226 227 228 229 230 231 232 233 234 235 236 237 238
! N T K V D K K V E P K S C
4468 aac acc aag gtg gac aaG AAA GTT GAG CCC AAA TCT TGT
ON-TQHCforw.....
!
! Poly His linker
! 139 140 141 142 143 144 145 146 147 148 149 150
! A A A H H H H H H G A A
4507 GCG GCC GCa cat cat cat cac cat cac ggg gcc gca
NotI.....
EagI.....
!
! 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
! E Q K L I S E E D L N G A A .
4543 gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gca tag
!
! Mature III----->...
! 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
! T V E S C L A K P H T E N S F
4588 act gtt gaa agt tgt tta gca aaa cct cat aca gaa aat tca ttt
!
! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
! T N V W K D D K T L D R Y A N
4633 act aac gtc tgg aaa gac gac aaa act tta gat cgt tac gct aac
!
! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
! Y E G C L W N A T G V V V C T
4678 tat gag ggc tgt ctg tgG AAT GCt aca ggc gtt gtg gtt tgt act
BsmI.....
!
! 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
! G D E T Q C Y G T W V P I G L
4723 ggt gac gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt
!
! 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
! A I P E N E G G G S E G G G S

4768 gct atc cct gaa aat gag ggt ggt ggc tct gag ggt ggc ggt tct
 ! 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
 ! E G G G S E G G G T K P P E Y
 4813 gag ggt ggc ggt tct gag ggt ggc ggt act aaa cct cct gag tac
 ! 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
 ! G D T P I P G Y T Y I N P L D
 4858 ggt gat aca cct att ccg ggc tat act tat atc aac cct ctc gac
 ! 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285
 ! G T Y P P G T E Q N P A N P N
 4903 ggc act tat ccg cct ggt act gag caa aac ccc gct aat cct aat
 ! 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
 ! P S L E E S Q P L N T F M F Q
 4948 cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
 ! BseRI..(2/2)
 ! 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315
 ! N N R F R N R Q G A L T V Y T
 4993 aat aat agg ttc cga aat agg cag ggt gca tta act gtt tat acg
 ! 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330
 ! G T V T Q G T D P V K T Y Y Q
 5038 ggc act gtt act caa ggc act gac ccc gtt aaa act tat tac cag
 ! 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345
 ! Y T P V S S K A M Y D A Y W N
 5083 tac act cct gta tca tca aaa gcc atg tat gac gct tac tgg aac
 ! 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
 ! G K F R D C A F H S G F N E D
 5128 ggt aaa ttc aga gac tgc gct ttc cat tct ggc ttt aat gaG GAT
 ! BamHI..
 ! 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375
 ! P F V C E Y Q G Q S S D L P Q
 5173 CCa ttc gtt tgt gaa tat caa ggc caa tcg tct gAC CTG Cct caa
 ! BamHI... BspMI...(2/2)
 ! 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390
 ! P P V N A G G G S G G G S G G
 5218 cct cct gtc aat gct ggc ggc tct ggt ggt ggt tct ggt ggc
 ! 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405
 ! G S E G G G S E G G G S E G G
 5263 ggc tct gag ggt ggc ggc tct gag ggt ggc ggt tct gag ggt ggc
 ! 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420
 ! G S E G G G S G G G S G S G D
 5308 ggc tct gag ggt ggc ggt tcc ggt ggc ggc tcc ggt tcc ggt gat

!
 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435
 F D Y E K M A N A N K G A M T
 5353 ttt gat tat gaa aaa atg gca aac gct aat aag ggg gct atg acc
 !
 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450
 E N A D E N A L Q S D A K G K
 5398 gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc aaa
 !
 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465
 L D S V A T D Y G A A I D G F
 5443 ctt gat tct gtc gct act gat tac ggt gct gct ATC GAT ggt ttc
 BspDI..
 !
 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480
 I G D V S G L A N G N G A T G
 5488 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt
 !
 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495
 D F A G S N S Q M A Q V G D G
 5533 gat ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt
 !
 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510
 D N S P L M N N F R Q Y L P S
 5578 gat aat tca cct tta atg aat aat ttc cgt caa tat tta cct tct
 !
 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525
 L P Q S V E C R P Y V F G A G
 5623 ttg cct cag tcg gtt gaa tgt cgc cct tat gtc ttt ggc gct ggt
 !
 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540
 K P Y E F S I D C D K I N L F
 5668 aaa cCA TAT Gaa ttt tct att gat tgt gac aaa ata aac tta ttc
 NdeI....
 !
 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555
 R G V F A F L L Y V A T F M Y
 5713 cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat
 !
 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570
 V F S T F A N I L R N K E S .
 5758 gta ttt tcg acg ttt gct aac ata ctg cgt aat aag gag tct taa
 !
 571
 !
 5803 taa GAATTTC
 EcoRI.
 5812 actggccgt cggttacaa cgtcgtgact gggaaaaccc tggcggttacc caacttaatc
 5871 gcctgcagc acatccccct ttcgcccagct ggcgtaatag cgaagaggcc cgcacCGATC
 Pvul..
 5931 Gccctccca acagtTGCAGC Agcctgaatg gcgaatGGCG CCtgcgtcggttacc tttttctcc
 ...PvuI... (3/3) FspI... (2/2) KasI... (2/2)
 5991 ttacgcatct gtgcggatt tcacaccgca tataaattgt aaacgttaat attttgtaa

6051 aattcgcgtt aaattttgt taaatcagct catttttaa ccaataggcc gaaatcgca
6111 aaatcccTTA TAAataaaaa gaatagcccg agatagggtt gagtgttgtt ccagtttgg
! PsiI...
6171 acaagagtcc actattaaag aacgtggact ccaacgtcaa agggcgaaaa accgtctatc
6231 agggcgatgg ccCACtacGT Gaaccatcac ccaaatcaag tttttgggg tcgaggtgcc
! DralIII....
6291 gtaaaggact aaatcggAAC cctaaaggGA gccccgatt tagagctGA cggggaaaGC
! NgoMIV..
6351 CGGCgaacgt ggcgagaaAG gaaggGAAG aagcgaaAGG agcgggcgt agggcgctgg
! ..NgoMIV.(2/2)
6411 caagtgttagc ggtcacgcgtc cgcgtAACCA ccacacccgc cgcgttaat ggcgcgtac
6471 agggcgctgtatgggtgc ttgacgggt gcagtcgtacataatctgc tctgatgcc
6531 catagttaaAG ccagccccGA caccCGccAA caccCGctGA cgcgcctGA cgggcttgc
6591 tgctcccgGC atccgcttac agacaagctG tgaccgttc cgggagctgc atgtgtcaga
6651 ggTTTcacc gtcatcacCG aaacgcgcga

Please delete Table 30 and replace it with the following table:

Table 30: Oligonucleotides used to clone CDR1/2 diversity

All sequences are 5' to 3'.

1) ON_CD1Bsp, 30 bases **(SEQ ID NO: 528)**

A c c T c A c T g g c T T c c g g A
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

T T c A c T T c T c T
19 20 21 22 23 24 25 26 27 28 29 30

2) ON_Br12, 42 bases **(SEQ ID NO: 529)**

A g A A A c c c A c T c c A A A c c
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

T T T A c c A g g A g c T T g g c g
19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

A A c c c A
37 38 39 40 41 42

3) ON_CD2Xba, 51 bases **(SEQ ID NO: 530)**

g g A A g g c A g T g A T c T A g A
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

g A T A g T g A A g c g A c c T T T
19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

A A c g g A g T c A g c A T A
37 38 39 40 41 42 43 44 45 46 47 48 49 50 51

4) ON_BotXba, 23 bases **(SEQ ID NO: 531)**

g g A A g g c A g T g A T c T A g A
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

g A T A g
19 20 21 22 23

Please delete Table 31 and replace it with the following table:

Table 31: Bridge/Extender Oligonucleotides

(SEQ ID NOS 532-546, respectively in order of appearance)

ON_Lam1aB7 (rc)	GTGCTGACTCAGCCACCCCTC.	20
ON_Lam2aB7 (rc)	GCCCTGACTCAGCCCTGCCTC.	20
ON_Lam31B7 (rc)	GAGCTGACTCAGGACCCTGC.	20
ON_Lam3rB7 (rc)	GAGCTGACTCAGCCACCCCTC.	20
ON_LamHf1cBrg (rc)	CCTCGACAGCGAAGTGCACAGAGCGTCTTGACTCAGCC.....	38
ON_LamHf1cExt	CCTCGACAGCGAAGTGCACAGAGCGTCTTG.....	30
ON_LamHf2b2Brg (rc)	CCTCGACAGCGAAGTGCACAGAGCGCTTTGACTCAGCC.....	38
ON_LamHf2b2Ext	CCTCGACAGCGAAGTGCACAGAGCGCTTTG.....	30
ON_LamHf2dBrg (rc)	CCTCGACAGCTAAGTGCACAGAGCGCTTTGACTCAGCC.....	38
ON_LamHf2dExt	CCTCGACAGCGAAGTGCACAGAGCGCTTTG.....	30
ON_LamHf31Brg (rc)	CCTCGACAGCGAAGTGCACAGAGCGAATTGACTCAGCC.....	38
ON_LamHf31Ext	CCTCGACAGCGAAGTGCACAGAGCGAATTG.....	30
ON_LamHf3rBrg (rc)	CCTCGACAGCGAAGTGCACAGTACGAATTGACTCAGCC.....	38
ON_LamHf3rExt	CCTCGACAGCGAAGTGCACAGTACGAATTG.....	30
ON_lamPlePCR	CCTCGACAGCGAAGTGCACAG.....	21
Consensus			

Please delete Table 32 and replace it with the following table:

Table 32: Oligonucleotides used to make SSDNA locally double-stranded

(SEQ ID NOS 548-552, respectively in order of appearance)

Adapters (8)

H43HF3.1?02#1	5'-cc gtg tat tac tgt gcg aga g-3'
H43.77.97.1-03#2	5'-ct gtg tat tac tgt gcg aga g-3'
H43.77.97.323#22	5'-cc gta tat tac tgt gcg aaa g-3'
H43.77.97.330#23	5'-ct gtg tat tac tgt gcg aaa g-3'
H43.77.97.439#44	5'-ct gtg tat tac tgt gcg aga c-3'
H43.77.97.551#48	5'-cc atg tat tac tgt gcg aga c-3'

Please delete Table 33 and replace it with the following table:

Table 33: Bridge/extender pairs

Bridges (2)

H43.XABr1

5'gggtgtagtgaTCTAGtgcacaactctaagaataactctctacttgcgagatgaacagCTTtAGggc
tgaggacaCTGCAGtctactattgtgcgaga-3' **(SEQ ID NO: 553)**

H43.XABr2

5'gggtgtagtgaTCTAGtgcacaactctaagaataactctctacttgcgagatgaacagCTTtAGggc
tgaggacaCTGCAGtctactattgtgcgaaa-3' **(SEQ ID NO: 554)**

Extender

H43.XAExt

5'ATAgTAgAcTgcAgTgTccTcAgccCTTAAGcTgTTcATcTgcAAGTAgAgAgTATTcTTAgA
gTTgTcTcTAgATcAcTAcAcc-3' **(SEQ ID NO: 555)**

Please delete Table 34 and replace it with the following table:

Table 34: PCR primers

Primers

H43.XAPCR2	gactgggTgTAgTgATcTAg	<u>(SEQ ID NO: 556)</u>
Hucmnest	cttttcttgttgcgttgggtg	<u>(SEQ ID NO: 557)</u>

Please delete Table 36 and replace it with the following table:

```
! Table 36: Annotated sequence of CJR DY3F7 (CJR-A05) 10251 bases
!
! Non-cutters
!
!BclI Tgatca      BsiWI Cgtacg      BssSI Cacgag
!BstZ17I GTAtac   BtrI CACgtg      EcoRV GATatc
!FseI GGCGGcc     HpaI GTTaac      MluI Acgcgt
!PmeI GTTTaaac    PmlI CACgtg      PpuMI RGgwccy
!RsrII CGgwccg   SapI GCTCTTC     SexAI Accwgg
!SgfI GCGATcgc   SgrAI CRccggg     SphI GCATGc
!StuI AGGcct      XmaI Cccggg
!
! cutters
!
! Enzymes that cut from 1 to 4 times and other features
!
!End of genes II and X          829
!Start gene V                   843
!BsrGI Tgtaca                 1   1021
!BspMI Nnnnnnnnnngcaggt      3   1104  5997  9183
(SEQ ID NO: 558)
! - " - ACCTGCNNNNn          1   2281
(SEQ ID NO: 559)
!End of gene V                 1106
!Start gene VII                1108
!BsaBI GATNNnnatc            2   1149  3967
(SEQ ID NO: 560)
!Start gene IX                 1208
!End gene VII                  1211
!SnaBI TACgtta                2   1268  7133
!BspHI Tcatga                 3   1299  6085  7093
!Start gene VIII                1301
!End gene IX                   1304
!End gene VIII                 1522
!Start gene III                  1578
!EagI Cggccg                  2   1630  8905
!XbaI Tctaga                  2   1643  8436
!KasI Ggcgcc                  4   1650  8724  9039  9120
!BsmI GAATGCN                 2   1769  9065
!BseRI GAGGAGNNNNNNNNNN      2   2031  8516
(SEQ ID NO: 561)
! - " - NNnnnnnnnnctcctc      2   7603  8623
(SEQ ID NO: 562)
!AlwNI CAGNNNctg              3   2210  8072  8182
```

!BspDI ATcgat	2	2520	9883		
!NdeI CAtatg	3	2716	3796	9847	
!End gene III		2846			
!Start gene VI		2848			
!AfeI AGCgct	1	3032			
!End gene VI		3187			
!Start gene I		3189			
!EarI CTCTTCNnnn	2	4067	9274		
<u>(SEQ ID NO: 563)</u>					
!-"- Nnnnnngaagag	2	6126	8953		
<u>(SEQ ID NO: 564)</u>					
!PacI TTAATTaa	1	4125			
!Start gene IV		4213			
!End gene I		4235			
!BsmFI Nnnnnnnnnnnnnnnngtccc	2	5068	9515		
<u>(SEQ ID NO: 565)</u>					
!MscI TGGcca	3	5073	7597	9160	
!PstI TTAtaa	2	5349	5837		
!End gene IV		5493			
!Start ori		5494			
!NgoMIV Gccggc	3	5606	8213	9315	
!BanII GRGCYC	4	5636	8080	8606	8889
!DraIII CACNNNgtg	1	5709			
!DrdI GACNNNNnngtc	1	5752			
<u>(SEQ ID NO: 566)</u>					
!AvaI Cycgrg	2	5818	7240		
!PvuII CAGctg	1	5953			
!BsmBI CGTCTCNnnnn	3	5964	8585	9271	
<u>(SEQ ID NO: 567)</u>					
!End ori region		5993			
!BamHI Ggatcc	1	5994			
!HindIII Aagctt	3	6000	7147	7384	
!BciVI GTATCCNNNNNN	1	6077			
<u>(SEQ ID NO: 568)</u>					
!Start bla		6138			
!Eco57I CTGAAG	2	6238	7716		
!SpeI Actagt	1	6257			
!BcgI gcannnnnntcg	1	6398			
<u>(SEQ ID NO: 569)</u>					
!ScaI AGTact	1	6442			
!PvuI CGATcg	1	6553			
!FspI TGCgca	1	6700			
!BglI GCCNNNNNnggc	3	6801	8208	8976	
<u>(SEQ ID NO: 570)</u>					
!BsaI GGTCTCNnnnn	1	6853			
<u>(SEQ ID NO: 571)</u>					
!AhdI GACNNNNnngtc	1	6920			
<u>(SEQ ID NO: 572)</u>					
!Eam1105I GACNNNNnngtc	1	6920			
<u>(SEQ ID NO: 573)</u>					
!End bla		6998			
!AccI GTmkac	2	7153	8048		
!HincII GTYrac	1	7153			
!SalI Gtcgac	1	7153			
!XbaI Ctcgag	1	7240			
!Start PlacZ region		7246			
!End PlacZ region		7381			
!PflMI CCANNNNntgg	1	7382			

(SEQ ID NO: 574)

!RBS1		7405	
!start M13-iii signal seq for LC		7418	
!ApaLI Gtgcac	1	7470	
!end M13-iii signal seq		7471	
!Start light chain kappa L20:JK1		7472	
!PflFI GACNNnngtc	3	7489	8705 9099
!SbfI CCTGCAGg	1	7542	
!PstI CTGCAG	1	7543	
!KpnI GGTACc	1	7581	
!XcmI CCANNNNNnnnntgg	2	7585	9215

(SEQ ID NO: 575)

!NsiI ATGCAt	2	7626	9503
!BsgI ctgcac	1	7809	
!BbsI gtcttc	2	7820	8616
!BlpI GCtnagc	1	8017	
!EspI GCtnagc	1	8017	
!EcoO109I RGgnccy	2	8073	8605
!Ecl136I GAGctc	1	8080	
!SacI GAGCTc	1	8080	
!End light chain		8122	
!AscI GGcgcgcc	1	8126	
!BssHII Gcgcgcc	1	8127	
!RBS2		8147	
!SfiI GGCCNNNNnggcc	1	8207	

(SEQ ID NO: 576)

!NcoI Ccatgg	1	8218	
!Start 3-23, FR1		8226	
!MfeI Caattg	1	8232	
!BspEI Tccgga	1	8298	
!Start CDR1		8316	
!Start FR2		8331	
!BstXI CCANNNNNntgg	2	8339	8812

(SEQ ID NO: 577)

!EcoNI CCTNNnnnagg	2	8346	8675
--------------------	---	------	------

(SEQ ID NO: 578)

!Start FR3		8373	
!XbaI Tctaga	2	8436	1643
!AflII Cttaag	1	8480	
!Start CDR3		8520	
!AatII GACGTc	1	8556	
!Start FR4		8562	
!PshAI GACNNnngtc	2	8573	9231

(SEQ ID NO: 579)

!BstEII Ggttnacc	1	8579	
!Start CH1		8595	
!ApaI GGGCCc	1	8606	
!Bsp120I Gggccc	1	8606	
!PspOMI Gggccc	1	8606	
!AgeI Accggt	1	8699	
!Bsu36I CCtnagg	2	8770	9509
!End of CH1		8903	
!NotI GCggccgc	1	8904	
!Start His6 tag		8913	

(SEQ ID NO: 12)

!Start cMyc tag		8931	
!Amber codon		8982	
!NheI Gctagc	1	8985	

!Start M13 III Domain 3	8997
!NruI TCGcga	1 9106
!BstBI TTcgaa	1 9197
!EcoRI Gaattc	1 9200
!XcmI CCANNNNNnnnntgg	1 9215
(SEQ ID NO: 580)	
!BstAPI GCANNNNntgc	1 9337
(SEQ ID NO: 581)	
!SacII CCGCgg	1 9365
!End IIIstump anchor	9455
!AvrII Cctagg	1 9462
!trp terminator	9470
!SwaI ATTTaaat	1 9784
!Start gene II	9850
!BglII Agatct	1 9936

(SEQ ID NO: 582)

```

1 aat gct act act att agt aga att gat gcc acc ttt tca gct cgc gcc
! gene ii continued
49 cca aat gaa aat ata gct aaa cag gtt att gac cat ttg cga aat gta
97 tct aat ggt caa act aaa tct act cgt tcg cag aat tgg gaa tca act
145 gtt aTa tgg aat gaa act tcc aga cac cgt act tta gtt gca tat tta
193 aaa cat gtt gag cta cag caT TaT att cag caa tta agc tct aag cca
241 tcc gca aaa atg acc tct tat caa aag gag caa tta aag gta ctc tct
289 aat cct gac ctg ttg gag ttt gct tcc ggt ctg gtt cgc ttt gaa gct
337 cga att aaa acg cga tat ttg aag tct ttc ggg ctt cct ctt aat ctt
385 ttt gat gca atc cgc ttt gct tct gac tat aat agt cag ggt aaa gac
433 ctg att ttt gat tta tgg tca ttc tcg ttt tct gaa ctg ttt aaa gca
481 ttt gag ggg gat tca ATG aat att tat gac gat tcc gca gta ttg gac
! Start gene x, ii continues
529 gct atc cag tct aaa cat ttt act att acc ccc tct ggc aaa act tct
577 ttt gca aaa gcc tct cgc tat ttt ggt tat cgt cgt ctg gta aac
625 gag ggt tat gat agt gtt gct ctt act atg cct cgt aat tcc ttt tgg
673 cgt tat gta tct gca tta gtt gaa tgt ggt att cct aaa tct caa ctg
721 atg aat ctt tct acc tgt aat aat gtt gtt ccg tta gtt cgt ttt att
769 aac gta gat ttt tct tcc caa cgt cct gac tgg tat aat gag cca gtt
817 ctt aaa atc gca TAA
! End X & II
832 ggtaattca ca

```

(SEQ ID NO: 626)

M1	E5	Q10	T15
843 ATG att aaa gtt gaa att aaa cca tct caa gcc caa ttt act act cgt			
Start gene V			
S17	S20	P25	E30
891 tct ggt gtt tct cgt cag ggc aag cct tat tca ctg aat gag cag ctt			
V35	E40	V45	
939 tgt tac gtt gat ttg ggt aat gaa tat ccg gtt ctt gtc aag att act			
D50	A55	L60	
987 ctt gat gaa ggt cag cca gcc tat gcg cct ggt cTG*TAC Acc gtt cat			
BsrGI...			
L65	V70	S75	R80
1035 ctg tcc tct ttc aaa gtt ggt cag ttc ggt tcc ctt atg att gac cgt			
P85 K87 end of V			

```

1083 ctg cgc ctc gtt ccg gct aag TAA C
!
1108 ATG gag cag gtc gcg gat ttc gac aca att tat cag gcg atg
! Start gene VII
!
1150 ata caa atc tcc gtt gta ctt tgt ttc gcg ctt ggt ata atc
!
VII and IX overlap.
! ..... S2 V3 L4 V5 (SEQ ID NO: 621) S10
1192 gct ggg ggt caa agA TGA gt gtt tta gtg tat tct ttT gcc tct ttc
gtt
!
End VII
| start IX
! L13 W15 G20 T25
E29
1242 tta ggt tgg tgc ctt cgt agt ggc att acg tat ttt acc cgt tta atg
gaa
!
1293 act tcc tc
!
! ..... stop of IX, IX and VIII overlap by four bases
1301 ATG aaa aag tct tta gtc ctc aaa gcc tct gta gcc gtt gct acc ctc
! Start signal sequence of viii.
!
1349 gtt ccg atg ctg tct ttc gct gct gag ggt gac gat ccc gca aaa gcg
! mature VIII --->
1397 gcc ttt aac tcc ctg caa gcc tca gcg acc gaa tat atc ggt tat gcg
1445 tgg gcg atg gtt gtt gtc att
1466 gtc ggc gca act atc ggt atc aag ctg ttt aag
!
! bases 1499-1539 are probable promoter for iii
1499 aaa ttc acc tcg aaa gca ! 1515
! ..... -35 ..
!
1517 agc tga taaaccgat acaattaaag gtcctttt
! ..... -10 ...
!
1552 gagcctttt ttt GGAGAt ttt ! S.D. uppercase, there may be 9 Ts
!
<----- III signal sequence ----->
(SEQ ID NO: 583)
!
! M K K L L F A I P L V V P F
1574 caac GTG aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc !
1620
!
! Y S G A A E S H L D G A
1620 tat tct ggc gCG GCC Gaa tca caT CTA GAc ggc gcc
! EagI.... XbaI....
!
! Domain 1 -----
! A E T V E S C L A
1656 gct gaa act gtt gaa agt tgt tta gca
!
! K S H T E I S F T N V W K D D K
T
1683 aaA Tcc cat aca gaa aat tca ttt aCT AAC GTC TGG AAA GAC GAC AAA
ACt
!

```

!
L D R Y A N Y E G S L W N A T G
V

1734 tta gat cgt tac gct aac tat gag ggC tgt ctg tgG AAT GCt aca ggc
gtt

!
BsmI....

!
V V C T G D E T Q C Y G T W V P
I

1785 gta gtt tgt act ggt GAC GAA ACT CAG TGT TAC GGT ACA TGG GTT cct
att

!
G L A I P E N
1836 ggg ctt gct atc cct gaa aat

!
L1 linker -----
E G G G S E G G G S
1857 gag ggt ggt ggc tct gag ggt ggc ggt tct

!
E G G G S E G G G T
1887 gag ggt ggc ggt tct gag ggt ggc ggt act

!
Domain 2 -----
1917 aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat atc
aac
1968 cct ctc gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat
cct
2019 aat cct tct ctt GAG GAG tct cag cct ctt aat act ttc atg ttt cag
aat

!
BseRI..
2070 aat agg ttc cga aat agg cag ggg gca tta act gtt tat acg ggc act
2118 gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act cct
2166 gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttC AGA
!
AlwNI
2214 GAC TGc gct ttc cat tct ggc ttt aat gaG gat TTa ttT gtt tgt gaa
!
AlwNI
2262 tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct

!
2307 ggc ggc ggc tct
!
start L2

2319 ggt ggt ggt tct
2331 ggt ggc ggc tct
2343 gag ggt ggt ggc tct gag gga ggc ggt tcc
2373 ggt ggc tct ggt ! end L2

!
Many published sequences of M13-derived phage have a longer linker
than shown here by repeats of the EGGGS (SEQ ID NO: 589) motif two
more times.

!
Domain 3
(SEQ ID NO: 584)

S G D F D Y E K M A N A N K G A
2388 tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct

!
M T E N A D E N A L Q S D A K G
2436 atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc

!

! K L D S V A T D Y G A A M D G F
 ! 2484 aaa ctt gat tct gtc gct act gat tac ggt gct gct gat ggt ttc
 !
 ! I G D V S G L A N G N G A T G D
 ! 2532 att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat
 !
 ! F A G S N S Q M A Q V G D G D N
 ! 2580 ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat
 !
 ! S P L M N N F R Q Y L P S L P Q
 ! 2628 tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa
 !
 ! S V E C R P F V F G A G K P Y E
 ! 2676 tcg gtt gaa tgt cgc cct ttt gtc ttt Ggc gct ggt aaa cca tat gaa
 !
 ! F S I D C D K I N L F R
 ! 2724 ttt tct att gat tgt gac aaa ata aac tta ttc cgt
 ! End Domain 3
 !
 ! G V F A F L L Y V A T F M Y V F140
 ! 2760 ggt gtc ttt gcg ttt ctt tta tat gtt gtc acc ttt atg tat gta ttt
 ! start transmembrane segment
 !
 ! S T F A N I L
 ! 2808 tct acg ttt gct aac ata ctg
 !
 ! R N K E S
 ! 2829 cgt aat aag gag tct TAA ! stop of iii
 ! Intracellular anchor.
 ! (SEQ ID NO: 585)
 ! M1 P2 V L L5 G I P L L10 L R F L G15
 ! 2847 tc ATG cca gtt ctt ttg ggt att ccg tta ttg cgt ttc ctc ggt
 ! Start VI
 !
 ! 2894 ttc ctt ctg gta act ttg ttc ggc tat ctg ctt act ttt ctt aaa aag
 ! 2942 ggc ttc ggt aag ata gct att gct att tca ttg ttt ctt gct ctt att
 ! 2990 att ggg ctt aac tca att ctt gtg ggt tat ctc tct gat att agc gct
 ! 3038 caa tta ccc tct gac ttt gtt cag ggt gtt cag tta att ctc ccg tct
 ! 3086 aat gcg ctt ccc tgt ttt tat gtt att ctc tct gta aag gct gct att
 ! 3134 ttc att ttt gac gtt aaa caa aaa atc gtt tct tat ttg gat tgg gat
 !
 ! M1 A2 V3 F5 L10 G13
 ! 3182 aaa TAA t ATG gct gtt tat ttt gta act ggc aaa tta ggc tct gga
 ! end VI Start gene I
 !
 ! (SEQ ID NO: 586)
 ! K T L V S V G K I Q D K I V A
 ! 3228 aag acg ctc gtt agc gtt ggt aag att cag gat aaa att gta gct
 !
 ! G C K I A T N L D L R L Q N L
 ! 3273 ggg tgc aaa ata gca act aat ctt gat tta agg ctt caa aac ctc
 !
 ! P Q V G R F A K T P R V L R I
 ! 3318 ccg caa gtc ggg agg ttc gct aaa acg cct cgc gtt ctt aga ata
 !
 ! P D K P S I S D L L A I G R G
 ! 3363 ccg gat aag cct tct ata tct gat ttg ctt gct att ggg cgc ggt

```

!      N   D   S   Y   D   E   N   K   N   G   L   L   V   L   D
3408 aat gat tcc tac gat gaa aat aaa aac ggc ttg ctt gtt ctc gat
!
!      E   C   G   T   W   F   N   T   R   S   W   N   D   K   E
3453 gag tgc ggt act tgg ttt aat acc cgt tct tgg aat gat aag gaa
!
!      R   Q   P   I   I   D   W   F   L   H   A   R   K   L   G
3498 aga cag ccg att att gat tgg ttt cta cat gct cgt aaa tta gga
!
!      W   D   I   I   F   L   V   Q   D   L   S   I   V   D   K
3543 tgg gat att att ttt ctt gtt cag gac tta tct att gtt gat aaa
!
!      Q   A   R   S   A   L   A   E   H   V   V   Y   C   R   R
3588 cag gcg cgt tct gca tta gct gaa cat gtt gtt tat tgt cgt cgt
!
!      L   D   R   I   T   L   P   F   V   G   T   L   Y   S   L
3633 ctg gac aga att act tta cct ttt gtc ggt act tta tat tct ctt
!
!      I   T   G   S   K   M   P   L   P   K   L   H   V   G   V
3678 att act ggc tcg aaa atg cct ctg cct aaa tta cat gtt ggc gtt
!
!      V   K   Y   G   D   S   Q   L   S   P   T   V   E   R   W
3723 gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg
!
!      L   Y   T   G   K   N   L   Y   N   A   Y   D   T   K   Q
3768 ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag
!
!      A   F   S   S   N   Y   D   S   G   V   Y   S   Y   L   T
3813 gct ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg
!
!      P   Y   L   S   H   G   R   Y   F   K   P   L   N   L   G
3858 cct tat tta tca cac ggt cgg tat ttc aaa cca tta aat tta ggt
!
!      Q   K   M   K   L   T   K   I   Y   L   K   K   F   S   R
3903 cag aag atg aaa tta act aaa ata tat ttg aaa aag ttt tct cgc
!
!      V   L   C   L   A   I   G   F   A   S   A   F   T   Y   S
3948 gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt aca tat agt
!
!      Y   I   T   Q   P   K   P   E   V   K   K   V   V   S   Q
3993 tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc tct cag
!
!      T   Y   D   F   D   K   F   T   I   D   S   S   Q   R   L
4038 acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt ctt
!
!      N   L   S   Y   R   Y   V   F   K   D   S   K   G   K   L
4083 aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa TTA
!                                         PacI
!
!      I   N   S   D   D   L   Q   K   Q   G   Y   S   L   T   Y
4128 ATT AAt agc gac gat tta cag aag caa ggt tat tca ctc aca tat
!                                         PacI
!
!      i   I   D   L   C   T   V   S   I   K   K   G   N   S   N   E
4173   att gat tta tgt act gtt tcc att aaa aaa ggt aat tca aAT Gaa
!                                         Start IV
! (SEQ ID NO: 527)

```

! i I V K C N .End of I
! iv L3 L N5 V I7 N F V10
4218 att gtt aaa tgt aat TAA T TTT GTT
! IV continued....
4243 ttc ttg atg ttt gtt tca tca tct tct ttt gct cag gta att gaa atg
4291 aat aat tcg cct ctg cgc gat ttt gta act tgg tat tca aag caa tca
4339 ggc gaa tcc gtt att gtt tct ccc gat gta aaa ggt act gtt act gta
4387 tat tca tct gac gtt aaa cct gaa aat cta cgc aat ttc ttt att tct
4435 gtt tta cgt gca aat aat ttt gat atg gta ggt tcT aAC cct tcc atT
4483 att cag aag tat aat cca aac aat cag gat tat att gat gaa ttg cca
4531 tca tct gat aat cag gaa tat gat gat aat tcc gct cct tct ggt ggt
4579 ttc ttt gtt ccg caa aat gat aat gtt act caa act ttt aaa att aat
4627 aac gtt cgg gca aag gat tta ata cga gtt gtc gaa ttg ttt gta aag
4675 tct aat act tct aaa tcc tca aat gta tta tct att gac ggc tct aat
4723 cta tta gtt gtt agt gcT cct aaa gat att tta gat aac ctt cct caa
4771 ttc ctt tcA act gtt gat ttg cca act gac cag ata ttg att gag ggt
4819 ttg ata ttt gag gtt cag caa ggt gat gct tta gat ttt tca ttt gct
4867 gct ggc tct cag cgt ggc act gtt gca ggc ggt gtt aat act gac cgc
4915 ctc acc tct gtt tta tct tct gct ggt ggt tcg ttc ggt att ttt aat
4963 ggc gat gtt tta ggg cta tca gtt cgc gca tta aag act aat agc cat
5011 tca aaa ata ttg tct gtg cca cgt att ctt acg ctt tca ggt cag aag
5059 ggt tct atc tct gtT GGC CAG aat gtc cct ttt att act ggt cgt gtg
! MscI....
5107 act ggt gaa tct gcc aat gta aat aat cca ttt cag acg att gag cgt
5155 caa aat gta ggt att tcc atg agc gtt ttt cct gtt gca atg gct ggc
5203 ggt aat att gtt ctg gat att acc agc aag gcc gat agt ttg agt tct
5251 tct act cag gca agt gat gtt att act aat caa aga agt att gct aca
5299 acg gtt aat ttg cgt gat gga cag act ctt tta ctc ggt ggc ctc act
5347 gat tat aaa aac act tct caG gat tct ggc gta ccg ttc ctg tct aaa
5395 atc cct tta atc ggc ctc ctg ttt agc tcc cgc tct gat tcT aac gag
5443 gaa agc acg tta tac gtg ctc gtc aaa gca acc ata gta cgc gcc ctg
5491 TAG cggcgcatt
! End IV
5503 aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct acacttgcca
gcgccttagc
5563 gcccgtcct ttgcgtttct tcccttcctt tctcgccacg ttcGCCGGCT
ttccccgtca
! NgoMI.
5623 agctctaaat cgggggctcc ctttagggtt ccgatttagt gctttacggc
acctcgaccc
5683 caaaaaactt gattgggtg atggttCACG TAGTGggcca tcgcctgtat
agacggtttt
! DraIII....
5743 tcgcctttG ACGTTGGAGT Ccacgttctt taatagtggaa ctcttgttcc
aaactggAAC
! DrdI.....
5803 aacactcaac cctatctcg gctattcttt tgatttataa gggattttgc
cgatttcgga
5863 accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg
cttgctgcaa
5923 ctctctcagg gccaggcggt gaagggaat CAGCTGttgc cCGTCTCact
ggtaaaaga
! PvuII. BsmBI.
5983 aaaaccaccc tGGATCC AAGCTT
! BamHI HindIII (1/2)
! Insert carrying bla gene
6006 gcaggtg gcactttcg gggaaatgtg cgcggAACCC

6043 ctatttgttt atttttctaa atacattcaa atatGTATCC gctcatgaga
 caataaccct

!
 BciVI

6103 gataaatgct tcaataatat tgaaaaAGGA AGAgt

!
 RBS.?...

!
 Start bla gene

6138 ATG agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg gca
 ttt

6189 tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta aaa gat
 gct

6240 gaa gat cag ttg ggC gcA CTA GTg ggt tac atc gaa ctg gat ctc aac
 agc

!
 SpeI....

!
 ApalI & BssSI Removed

6291 ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg
 agc

6342 act ttt aaa gtt ctg cta tgt GGC GcG Gta tta tcc cgt att gac gcc
 ggg

6393 caa gaG CAA CTC GGT CGc cgC ATA cAC tat tct cag aat gac ttg gtt
 gAG

!
 BcgI.....

ScaI

6444 TAC Tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga
 gaa

!
 ScaI.

6495 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta
 ctt

6546 ctg aca aCG ATC Gga gga ccg aag gag cta acc gct ttt ttg cac aac
 atg

!
 PvuI....

6597 ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa
 gcc

6648 ata cca aac gac gag cgt gac acc acg atg cct gta gca atg Gca aca
 acg

6699 tTG CGC Aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa
 caa

!
 FspI....

!

6750 tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc
 tcg

6801 GCC ctt ccG GCT ggc tgg ttt att gct gat aaa tct gga gcc ggt gag
 cgt

!
 BglI.....

6852 gGG TCT Cgc ggt atc att gca gca ctg ggg cca gat ggt aag ccc tcc
 cgt

!
 BsaI....

6903 atc gta gtt atc tac acG ACg ggg aGT Cag gca act atg gat gaa cga
 aat

!
 AhdI.....

6954 aga cag atc gct gag ata ggt gcc tca ctg att aag cat tgg TAA ctgt
 !
 stop

7003 cagaccaagt ttactcatat atactttaga ttgatttaaa acttcatttt
 taatttaaaa

7063 ggatcttaggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa
 cgtgagttt

7123 cgTTccactg tacgtaagac cccc

7147 AAGCTT GTCGAC tgaa tggcgaatgg cgctttgcct

!
 HindIII SalI..

```

!      (2/2)      HincII
7183 gggttccggc accagaagcg gtgccggaaa gctggctgga gtgcgatctt
!
! Start of Fab-display cassette, the Fab DSR-A05, selected for
! binding to a protein antigen.
!
7233 CCTGAcG CTCGAG
!      xBsU36I XhoI..
!
! PlacZ promoter is in the following block
!
7246                      cgcaacgc aattaatgtg agttagctca
7274      ctcattaggc accccaggct ttacacttta tgcttccggc tcgtatgttgc
7324      tgtgaaattg tgagcggata acaatttac acaggaaaca gctatgacca
7374      tgattacgCC AagcttTGGa gcctttttt tggagattttt caac
!
!      PflMI.....
!
!      Hind3. (there are 3)
!
! Gene iii signal sequence: (Amino acid sequence is SEQ ID NO: 587)
!
!      1   2   3   4   5   6   7   8   9   10  11  12  13  14  15
!      M   K   K   L   L   F   A   I   P   L   V   V   P   F   Y
7418      gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat
!
!      16  17  18          Start light chain (L20:JK1)
!      S   H   S   A   Q   D   I   Q   M   T   Q   S   P   A
7463      tct cac aGT GCA Caa gac atc cag atg acc cag tct cca gcc
!
!      ApaLI...
!
!      Sequence supplied by extender.....
!
!
!      T   L   S   L
7505      acc ctg tct ttg
!
!
!      S   P   G   E   R   A   T   L   S   C   R   A   S   Q   G
7517      tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag Ggt
!
!      V   S   S   Y   L   A   W   Y   Q   Q   K   P   G   Q   A
7562      gtt agc agc tac tta gcc tgg tac cag cag aaa cct ggc cag gct
!
!      P   R   L   L   I   Y   D   A   S   S   R   A   T   G   I
7607      ccc agg ctc ctc atc tat gAt gca tcc aAc agg gcc act ggc atc
!
!      P   A   R   F   S   G   S   G   P   G   T   D   F   T   L
7652      cca gCc agg ttc agt ggc agt ggg Cct ggg aca gac ttc act ctc
!
!      T   I   S   S   L   E   P   E   D   F   A   V   Y   Y   C
7697      acc atc agc agC ctA gag cct gaa gat ttt gca gtT tat tac tgt
!
!      Q   Q   R   S   W   H   P   W   T   F   G   Q   G   T   R
7742      cag cag CGt aAc tgg cat ccg tgg ACG TTC GGC CAA GGG ACC AAG
!
!      V   E   I   K   R   T   V   A   A   P   S   V   F   I   F
7787      gtg gaa atc aaa cga act gtg gCT GCA Cca tct gtc ttc atc ttc
!
!      BsgI.....
!
!
!      P   P   S   D   E   Q   L   K   S   G   T   A   S   V   V
7832      ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg
!
!      C   L   L   N   N   F   Y   P   R   E   A   K   V   Q   W
7877      tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg

```

!

! 7922 K V D N A L Q S G N S Q E S V
! aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc

!

! 7967 T E R D S K D S T Y S L S S T
! aca gag cgg gac agc aag gac agc acc tac agc ctc agc agc acc

!

! 8012 L T L S K A D Y E K H K V Y A
! ctg acG CTG AGC aaa gca gac tac gag aaa cac aaa gtc tac gcc
! EspI.....

!

! 8057 C E V T H Q G L S S P V T K S
! tgc gaa gtc acc cat cag ggc ctG AGC TCg ccc gtc aca aag agc
! SacI.....

!

! 8102 F N R G E C . .
! ttc aac agg gga gag tgt taa taa

!

! 8126 GGC GCG CCaattctat ttcaaGGAGA cagtcata
! AscI..... RBS2.

!

(Amino acid sequence is SEQ ID NO: 588)

! PelB signal sequence----- (22 codons) ----->

! 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
! M K Y L L P T A A A G L L L L
! 8160 atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc

!

! ... PelB signal-----> Start VH, FR1----->

! 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
! A A Q P A M A E V Q L L E S G
! 8205 gcG GCC cag ccG GCC atg gcc gaa gtt CAA TTG tta gag tct ggt
! SfiI..... MfeI...
! NcoI.....

!

! 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
! G G L V Q P G G S L R L S C A
! 8250 ggc ggt ctt gtt cag cct ggt ggt tct tta cgt ctt tct tgc gct

!

! ... FR1-----> CDR1-----> FR2----->

! 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
! A S G F T F S T Y E M R W V R
! 8295 gct TCC GGA ttc act ttc tct act tac gag atg cgt tgg gtt cgC
! BspEI..

BstXI...

!

! FR2-----> CDR2 ----->

! 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75
! Q A P G K G L E W V S Y I A P
! 8340 CAa gct ccT GGt aaa ggt ttg gag tgg gtt tct tat atc gct cct

BstXI.....

!

! ... CDR2-----> FR3----->

! 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
! S G G D T A Y A D S V K G R F
! 8385 tct ggt ggc gat act gct tat gct gac tcc gtt aaa ggt cgc ttc

!

! 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105
! T I S R D N S K N T L Y L Q M
! 8430 act atc TCT AGA gac aac tct aag aat act ctc tac ttg cag atg

!
 ! XbaI...
 ! Supplied by extender-----

!
 ! -----FR3----->
 ! 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 ! N S L R A E D T A V Y Y C A R
 ! 8475 aac agC TTA AGg gct gag gac act gca gtc tac tat tgt gcg agg
 !
 ! AflII...
 ! from extender----->

!
 ! CDR3----->
 ! FR4-->
 ! 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135
 ! R L D G Y I S Y Y G M D V W
 ! 8520 agg ctc gat ggc tat att tcc tac tac tac ggt atg GAC GTC tgg
 !
 ! AatII..
 !
 ! 136 137 138 139 140 141 142 143 144 145
 ! G Q G T T V T V S S
 ! 8565 ggc caa ggg acc acG GTC ACC gtc tca agc
 !
 ! BstEII...
 !
 ! CH1 of IgG1----->
 ! A S T K G P S V F P L A P S S
 ! 8595 gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc
 !
 ! K S T S G G T A A L G C L V K
 ! 8640 aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag
 !
 ! D Y F P E P V T V S W N S G A
 ! 8685 gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc
 !
 ! L T S G V H T F P A V L Q S S
 ! 8730 ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tcc TCA
 !
 ! Bsu36I.....
 !
 ! G L Y S L S S V V T V P S S S
 ! 8775 GGa ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc agc agc
 !
 ! Bsu36I.....
 !
 ! L G T Q T Y I C N V N H K P S
 ! 8820 ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc
 !
 ! N T K V D K K V E P K S C A A
 ! 8865 aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt GCG GCC
 !
 ! NotI.....
 !
 ! A H H H H H G A A E Q K L I
 ! 8910 GCa cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc
 !
 ! ..NotI.... H6 tag..... Myc-Tag.....
 !
 ! S E E D L N G A A q A S S A
 ! 8955 tca gaa gag gat ctg aat ggg gcc gca tag GCT AGC tct gct
 !
 ! Myc-Tag..... ... NheI...
 !
 ! Amber

```

! III'stump
!
! Domain 3 of III
-----
!
!      S   G   D   F   D   Y   E   K   M   A   N   A   N   K   G   A
8997 agt ggc gac ttc gac tac gag aaa atg gct aat gcc aac aaa GGC GCC
!      tcc  t  t  t  t  a  g      a  c  t  t  g  g  t
!W.T.

!
KasI...(2/4)
!
!      M   T   E   N   A   D   E   N   A   L   Q   S   D   A   K   G
9045 atG ACT GAG AAC GCT GAC GAG aat gct ttg caa agc gat gcc aag ggt
!      c  a  t  c  t  a  c  g  c  a  g  t  c  t  a  c
!W.T.

!
!      K   L   D   S   V   A   T   D   Y   G   A   A   I   D   G   F
9093 aag tta gac agc gTC GCG Acc gac tat GGC GCC gcc ATC GAc ggc ttt
!      a  c  t  t  t  c  t  t  c  t  t  t  t  t  c
!W.T.

!
NruI.... KasI...(3/4)
!
!      I   G   D   V   S   G   L   A   N   G   N   G   A   T   G   D
9141 atc ggc gat gtc agt ggt tTG GCC Aac ggc aac gga gcc acc gga gac
!      t  t  c  t  t  c  t  t  t  t  t  t  t  t  t
!W.T.

!
MscI...(3/3)
!
!      F   A   G   S   N   S   Q   M   A   Q   V   G   D   G   D   N
9189 ttc GCA GGT tcG AAT TCt cag atg gcC CAG GTT GGA GAT GGg gac aac
!      t  t  c  t  c  a  t  a  c  t  c  t  c  t  t  t
!W.T.

!
BspMI.. (2/2) XcmI.....
!
EcoRI...
!
!      S   P   L   M   N   N   F   R   Q   Y   L   P   S   L   P   Q
9237 agt ccg ctt atg aac aac ttt aga cag tac ctt ccg tct ctt ccg cag
!      tca  t  t  a  t  t  c  c  t  a  t  t  a  t  c  c  t  a
!W.T.

!
!      S   V   E   C   R   P   F   V   F   S   A   G   K   P   Y   E
9285 agt gtc gag tgc cgt cca ttc gtt ttc tct gcc ggc aag cct tac gag
!      tcg  t  a  t  c  t  t  c  t  agc  t  t  a  a  t  a
!W.T.

!
!      F   S   I   D   C   D   K   I   N   L   F   R
9333 ttc aGC Atc gac TGC gat aag atc aat ctt ttC CGC
!      t  t  t  t  t  c  a  a  c  t  a  c  t  !W.T.
!
BstAPI.....
!
SacII...
!
End Domain 3
!
!      G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F
9369 GGC gtt ttc gct ttc ttg cta tac gtc gct act ttc atg tac gtt ttc
!      t  c  t  g  t  c  t  a  t  t  c  c  t  t  a  t
!W.T.

!
start transmembrane segment
!

```

```

!
!      S   T   F   A   N   I   L   R   N   K   E   S
9417 aGC ACT TTC GCC AAT ATT TTA Cgc aac aaa gaa agc
!      tct   g   t   t   c   a c g   t   t   g   g tct !W.T.
!                                         Intracellular anchor.

!
!      .
9453      tag tga tct CCT AGG
!                                         AvrII..

!
!      9468 aag ccc gcc taa tga gcg ggc ttt ttt ttt ct  ggt
!                                         | Trp terminator
!                                         |
!      End Fab cassette
!
!      9503 ATGCAT CCTGAGG ccgat actgtcgctcg tccctcaaa ctggcagatg
!                                         NsiI.. Bsu36I. (3/3)
!      9551 cacggttacg atgcggccat ctacaccaac gtgacctatac ccattacgg
caatccggcg
!      9611 tttgttccca cggagaatcc gacgggttgt tactcgctca catttaatgt
tgatgaaagc
!      9671 tggctacagg aaggccagac gcgaattatt tttgatggcg ttcctattgg
ttaaaaaatg
!      9731 agctgattta acaaaaattt aaTgcgaatt ttaacaaaat attaacgtt
acaATTAAA
!
!      SwaI...
!      9791 Tatttgotta tacaatcttc ctgttttgg ggctttctg attatcaacc GGGGTACat
!      9850 ATG att gac atg cta gtt tta cga tta ccg ttc atc gat tct ctt gtt
tgc
!      Start gene II
!      9901 tcc aga ctc tca ggc aat gac ctg ata gcc ttt gtA GAT CTc tca aaa
ata
!
!                                         BglII...
!      9952 gct acc ctc tcc ggc atT aat tta tca gct aga acg gtt gaa tat cat
att
!      10003 gat ggt gat ttg act gtc tcc ggc ctt tct cac cct ttt gaa tct tta
cct
!      10054 aca cat tac tca ggc att gca ttt aaa ata tat gag ggt tct aaa aat
ttt
!      10105 tat cct tgc gtt gaa ata aag gct tct ccc gca aaa gta tta cag ggt
cat
!      10156 aat gtt ttt ggt aca acc gat tta gct tta tgc tct gag gct tta ttg
ctt
!      10207 aat ttt gct aat tct ttg cct tgc ctg tat gat tta ttg gat gtt !
!      gene II continues
!----- End of Table -----

```

Please delete Table 37 and replace it with the following table:

```

! Table 37: DNA seq of w.t. M13 gene iii
(Nucleotide sequenc is SEQ ID NO: 590; Amino acid sequence is SEQ ID
NO: 591)
!
!      1   2   3   4   5   6   7   8   9   10  11  12  13  14  15
!      fM   K   K   L   L   F   A   I   P   L   V   V   P   F   Y
1579  gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat

```

```

!     Signal sequence.....  

!  

!     16 17 18 19 20 21 22 23 24 25 26 27 28 29 30  

!     S H S A E T V E S C L A K P H  

! 1624 tct cac tcc gct gaa act gtt gaa agt tgt tta gca aaa ccc cat  

! Signal sequence> Domain 1-----  

!  

!     31 32 33 34 35 36 37 38 39 40 41 42 43 44 45  

!     T E N S F T N V W K D D K T L  

! 1669 aca gaa aat tca ttt act aac gtc tgg aaa gac gac aaa act tta  

! Domain 1-----  

!  

!     46 47 48 49 50 51 52 53 54 55 56 57 58 59 60  

!     D R Y A N Y E G C L W N A T G  

! 1714 gat cgt tac gct aac tat gag ggt tgt ctg tgG AAT GCt aca ggc  

!                                         BsmI....  

! Domain 1-----  

!  

!     61 62 63 64 65 66 67 68 69 70 71 72 73 74 75  

!     V V V C T G D E T Q C Y G T W  

! 1759 gtt gta gtt tgt act ggt gac gaa act cag tgt tac ggt aca tgg  

! Domain 1-----  

!  

!     76 77 78 79 80 81 82 83 84 85 86 87 88 89 90  

!     V P I G L A I P E N E G G G S  

! 1804 gtt cct att ggg ctt gct atc cct gaa aat gag ggt ggt ggc tct  

! Domain 1-----> Linker 1-----  

!  

!     91 92 93 94 95 96 97 98 99 100 101 102 103 104 105  

!     E G G S E G G G S E G G G T  

! 1849 gag ggt ggc ggt tct gag ggt ggc ggt tct gag ggt ggc ggt act  

! Linker 1----->  

!  

!     106 107 108 109 110 111 112 113 114 115 116 117 118 119 120  

!     K P P E Y G D T P I P G Y T Y  

! 1894 aaa cct cct gag tac ggt gat aca cct att ccg ggc tat act tat  

! Domain 2-----  

!  

!     121 122 123 124 125 126 127 128 129 130 131 132 133 134 135  

!     I N P L D G T Y P P G T E Q N  

! 1939 atc aac cct ctc gac ggc act taT CCG CCT ggt act gag caa aac  

!                                         EciI....  

! Domain 2-----  

!  

!     136 137 138 139 140 141 142 143 144 145 146 147 148 149 150  

!     P A N P N P S L E E S Q P L N  

! 1984 ccc gct aat cct aat cct tct ctt GAG GAG tct cag cct ctt aat  

!                                         BseRI..  

! Domain 2-----  

!  

!     151 152 153 154 155 156 157 158 159 160 161 162 163 164 165  

!     T F M F Q N N R F R N R Q G A  

! 2029 act ttc atg ttt cag aat aat agg ttc cga aat agg cag ggg gca  

! Domain 2-----  

!  

!     166 167 168 169 170 171 172 173 174 175 176 177 178 179 180  

!     L T V Y T G T V T Q G T D P V  

! 2074 tta act gtt tat acg ggc act gtt act caa ggc act gac ccc gtt

```

```

!
! Domain 2-----
!
! 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195
!   K   T   Y   Y   Q   Y   T   P   V   S   S   K   A   M   Y
2119 aaa act tat tac cag tac act cct gta tca tca aaa gcc atg tat
!
! Domain 2-----
!
! 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210
!   D   A   Y   W   N   G   K   F   R   D   C   A   F   H   S
2164 gac gct tac tgg aac ggt aaa ttC AGa gac TGc gct ttc cat tct
!                                         AlwNI.....
!
! Domain 2-----
!
! 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
!   G   F   N   E   D   P   F   V   C   E   Y   Q   G   Q   S
2209 ggc ttt aat gaG GAT CCa ttc gtt tgt gaa tat caa ggc caa tcg
!                                         BamHI...
!
! Domain 2-----
!
! 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
!   S   D   L   P   Q   P   P   V   N   A   G   G   G   S   G
2254 tct gac ctg cct caa cct cct gtc aat gct ggc ggc ggc tct ggt
!
! Domain 2-----> Linker 2-----
!
! 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
!   G   G   S   G   G   S   E   G   G   G   G   S   E   G   G
2299 ggt ggt tct ggt ggc ggc tct gag ggt ggt ggc tct gag ggt ggc
!
! Linker 2-----
!
! 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
!   G   S   E   G   G   G   S   E   G   G   G   S   G   G   G
2344 ggt tct gag ggt ggc ggc tct gag gga ggc ggt tcc ggt ggt ggc
!
! Linker 2-----
!
! 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285
!   S   G   S   G   D   F   D   Y   E   K   M   A   N   A   N
2389 tct ggt tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat
!
! Linker 2> Domain 3-----
!
! 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
!   K   G   A   M   T   E   N   A   D   E   N   A   L   Q   S
2434 aag ggg gct atg acc gaa aat gcc gat gaa aac gcg cta cag tct
!
! Domain 3-----
!
! 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315
!   D   A   K   G   K   L   D   S   V   A   T   D   Y   G   A
2479 gac gct aaa ggc aaa ctt gat tct gtc gct act gat tac ggt gct
!
! Domain 3-----
!
! 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330
!   A   I   D   G   F   I   G   D   V   S   G   L   A   N   G
2524 gct atc gat ggt ttc att ggt gac gtt tcc ggc ctt gct aat ggt
!
! Domain 3-----
!
! 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345
!   N   G   A   T   G   D   F   A   G   S   N   S   Q   M   A
2569 aat ggt gct act ggt gat ttt gct ggc tct aat tcc caa atg gct
!
! Domain 3-----

```

```

!
!      346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
!      Q      V      G      D      G      D      N      S      P      L      M      N      N      F      R
2614 caa gtc ggt gac ggt gat aat tca cct tta atg aat aat ttc cgt
!      Domain 3-----
!
!      361 362 363 364 365 366 367 368 369 370 371 372 373 374 375
!      Q      Y      L      P      S      L      P      Q      S      V      E      C      R      P      F
2659 caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct ttt
!      Domain 3-----
!
!      376 377 378 379 380 381 382 383 384 385 386 387 388 389 390
!      V      F      S      A      G      K      P      Y      E      F      S      I      D      C      D
2704 gtc ttt agc gct ggt aaa cca tat gaa ttt tct att gat tgt gac
!      Domain 3-----
!
!      391 392 393 394 395 396 397 398 399 400 401 402 403 404 405
!      K      I      N      L      F      R      G      V      F      A      F      L      L      Y      V
2749 aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt
!      Domain 3-----> Transmembrane segment-----
!
!      406 407 408 409 410 411 412 413 414 415 416 417 418 419 420
!      A      T      F      M      Y      V      F      S      T      F      A      N      I      L      R
2794 gcc acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt
!      Transmembrane segment-----> ICA--
!
!      421 422 423 424 425
!      N      K      E      S      .
2839 aat aag gag tct taa ! 2853
!      ICA-----> ICA = intracellular anchor
!
!----- End of Table
-----
```

Please delete Table 38 and replace it with the following table:

Table 38: Whole mature III anchor M13-III
derived anchor with recoded DNA

```

!
!      1      2      3
!      A      A      A  (SEQ ID NO: 594)
1      GCG  gcc  gca  (SEQ ID NO: 593)
!      NotI.....
!
!      4      5      6      7      8      9      10      11      12      13      14      15      16      17
!      H      H      H      H      H      H      G      A      A      E      Q      K      L      I
10     cat  cat  cat  cac  cat  cac  ggg  gcc  gca  gaa  caa  aaa  ctc  atc
!
!      18     19     20     21     22     23     24     25     26     27     28     29
!      S      E      E      D      L      N      G      A      A      .      A      S
52     tca  gaa  gag  gat  ctg  aat  ggg  gcc  gca  Tag  GCT  AGC
!      NheI...
!
!      30     31     32     33     34     35     36      37     38     39
!      D      I      N      D      D      R      M      A      S      T
88     GAT  ATC  aac  gat  gat  cgt  atg  gct  tct  act
!  (ON_G37bot)  [RC]  5'-c aac gat gat cgt atg gcg CAT Gct gcc gag aca g-3'
!  EcoRV..  (SEQ ID NO: 592)
```


a g c c a t a g g g a t a t t t g c t ! W.T.
 HgiAI... BsrGI...

194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
 V T Q G T D P V K T Y Y Q Y T
 580 |gtC|acc|caG|GGT|ACC|gaT|cCT|gtC|aaG|acC|taC|taT|caA|taT|acC|
 t t a c t c c t a t t c g c t ! W.T.
 KpnI...

209 210 211 212 213 214 215 216 217 218 219 220 221 222 223
 P V S S K A M Y D A Y W N G K
 625 |ccG|gtC|TCG|AGt|aaG|gcT|atg|taC|gaT|gcC|taT|tgg|aaT|ggC|aaG|
 t a atca a c t c t c c t a ! W.T.
 BsaI...
 XhoI...

224 225 226 227 228 229 230 231 232 233 234 235 236 237 238
 F R D C A F H S G F N E D P F
 670 |ttT|CgT|gaT|tgT|gcC|ttT|cac|AGC|ggT|ttC|aaC|gaa|gac|CCT|ttT|
 C A a C c t c t c t t G T a c ! W.T.

239 240 241 242 243 244 245 246 247 248 249 250 251 252 253
 V C E Y Q G Q S S D L P Q P P
 715 |gtC|tgC|gaG|taC|caG|ggT|cAG|AGT|AGC|gaT|TtA|ccG|caG|ccA|CCG|
 t t a t a c a t c t c c g t a t t ! W.T.
 DrdI...
 AgeI...

Domain 2-----> Linker 2----->
 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
 V N A G G G S G G G S G G G S
 760 |GTT|AAC|gcG|ggT|ggT|ggT|AGC|ggC|ggA|ggC|AGC|ggA|ggC|ggC|ggT|ggT|AGC|
 c t t c c t c t t t t t c c t c t ! W.T.

AgeI...
 HpaI...
 HincII.

Linker 2-----> Domain 3-->
 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
 E G G G S E G G G S G G S G
 805 |gaA|ggC|ggA|ggT|AGC|gaA|ggA|ggT|ggC|AGC|ggA|ggC|ggT|AGC|ggC|
 g t t c t c t g t c t c t g t c t c t t ! W.T.

-----Domain 3----->
 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298
 S G D F D Y E K M A N A N K G
 850 |AGT|ggC|gac|ttc|gac|tac|gag|aaa|atg|gct|aat|gcc|aac|aaa|GGC|
 tcc t t t t a g a c t t g g g ! W.T.
 KasI...

299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
 A M T E N A D E N A L Q S D A
 895 |GCC|atg|act|gag|aac|gct|gac|gaG|AAT|GCA|ctg|caa|agt|gat|gCC|
 t c a t c t a c g a g t c t c t ! W.T.
 KasI...
 BsmI...
 StyI...

314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
 K G K L D S V A T D Y G A A I
 940 |AAG|GGt|aag|tta|gac|agc|gTC|GCc|Aca|gac|tat|ggT|GCT|gcc|atc|
 a c a c t t t c t t t c t t ! W.T.

StyI...
 PflFI...

329 330 331 332 333 334 335 336 337 338 339 340 341 342 343
 D G F I G D V S G L A N G N G
 985 |gac|ggc|ttt|atc|ggc|gat|gtc|agt|ggT|ctg|gct|aac|ggc|aac|gga|
 t t c t t c t t c c t t t t t ! W.T.

```

344 345 346 347 348 349 350 351 352 353
A T G D F A G S N S
1030 |gcc|acc|gga|gac|ttc|GCA|GGT|tcG|AAT|TCt|
t t t t t c t c ! W.T.
BstBI...
EcoRI...
BspMI..

354 355 356 357 358 359 360 361 362 363
Q M A Q V G D G D N
1060 cag atg gcC CAG GTT GGA GAT GGg gac aac
a t a c t c t t t ! W.T.
XcmI.....
```

```

364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379
S P L M N N F R Q Y L P S L P Q
1090 agt ccg ctt atg aac aac ttt aga cag tac ctt ccg tct ctt ccg cag
tca t t a t c t a t t a t c c t a ! W.T.
```

```

380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395
S V E C R P F V F S A G K P Y E
1138 agt gtc gag tgc cgt cca ttc gtt ttc tct gcc ggc aag cct tac gag
tcg t a t c t c t a g c t t a a a t a ! W.T.
```

```

Domain 3----->
396 397 398 399 400 401 402 403 404 405 406 407
F S I D C D K I N L F R
1186 ttc aGC Atc gac TGC gat aag atc aat ctt ttC CGC
t tct t t c a a c t a t
BstAPI..... SacII...
```

```

transmembrane segment----->
408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423
G V F A F L L Y V A T F M Y V F
1222 GGc gtt ttc gct ttc ttg cta tac gtc gct act ttc atg tac gtt ttc
t c t g t c t t a t t c c t t a t ! W.T.
```

```

424 425 426 427 428 429 430 431 432 433 434 435
S T F A N I L R N K E S
1270 aGC ACT TTC GCC AAT ATT TTA Cgc aac aaa gaa agc
tct g t t c a c g t t g g tct ! W.T.
Intracellular anchor.
```

```

1306 tag tga tct CCT AGG
AvrII..
```

```

1321 aag ccc gcc taa tga gcg ggc ttt ttt ttt ct ggt
| Trp terminator |
```

```

End Fab cassette
----- End of Table -----
```

Please delete Table 39 and replace it with the following table:

Table 39: ONs to make deletions in III

Table 39. CDS of *lambda* and *lambda* ONs for use with *NheI*

N

(SEQ. ID. NO.: 595)

(SEQ ID NO.:
(ON G38bot)

5'-C GTT GAT ATC GCT AAG CTA TGC-3'

1 22

(ON_G29b0c) 5'-c gtt gat Atc gct Agc cta tgc-3' ! this is the reverse complement of 5'-gca tag gct agc gat atc aac g-3' NheI... scab...

```

(ON_G104top) 5'-g|ata|ggc|tta|gcT|aGC|ccg|gag|aac|gaa|gg-3'      ! 30
(SEQ ID NO: 596)
! Scab.....NheI... 104 105 106 107 108
(ON_G236top) 5'-c|ttt|cac|agc|ggt|ttc|GCT|AGC|gac|cct|ttt|gtc|tgc-3'      ! 37
(SEQ ID NO: 597)
! NheI... 236 237 238 239 240
(ON_G236tCS) 5'-c|ttt|cac|agc|ggt|ttc|GCT|AGC|gac|cct|ttt|gtc|Agc-
! NheI... 236 237 238 239 240
!          gag|tac|cag|ggt|c-3'  (SEQ ID NO: 598)
! 50

! ONs for use with SphiI G CAT Gc
(ON_X37bot) 5'-gAc TgT cTc ggc Agc ATg cgc cAT Acg ATc ATc gTT g-3' ! 37
(SEQ ID NO: 599)
! N D D R M A H A (SEQ ID NO: 601)
! (ON_X37bot)=[RC] 5'-c aac gat gat cgt atg gcGCAt Gct gcc gag aca gtc-3'
(SEQ ID NO: 600)
! SphiI....Scab.....
(ON_X104top) 5'-g|gtG ccg|ata|ggc|ttG|CAT|gCa|ccg|gag|aac|gaa|gg-3'      ! 36
(SEQ ID NO: 617)
! Scab.....SphiI.... 104 105 106 107 108
(ON_X236top) 5'-c|ttt|cac|agc|ggt|ttG|CaT|gCa|gac|cct|ttt|gtc|tgc-3'      ! 37
(SEQ ID NO: 602)
! SphiI.... 236 237 238 239 240
(ON_X236tCS) 5'-c|ttt|cac|agc|ggt|ttG|CaT|gCa|gac|cct|ttt|gtc|Agc-
! NheI... 236 237 238 239 240
!          gag|tac|cag|ggt|c-3'  (SEQ ID NO: 603)
! 50

```